

## Abstract

Species interactions are believed to play an important role in community structure, but detecting their influence in the co-occurrence patterns of observed communities has stymied ecologists for decades. While Markov networks (undirected graphical models also known as Markov random fields) represent a promising approach to this long-standing problem by isolating direct interactions from indirect ones, the methods ecologists have suggested for fitting these models are limited to small communities with about 20 species or fewer. Additionally, the methods that have been proposed so far do not account for environmental heterogeneity, and thus attempt to explain all of the co-occurrence patterns in ecological data sets with species interactions. In this paper, I introduce stochastic approximation as an alternative method for fitting these models that addresses both of these problems, making it feasible to use Markov networks in cases where each species responds to multiple abiotic factors and hundreds of competitors or mutualists. While stochastic approximation does introduce some sampling noise during the optimization process, it still converges to the maximum likelihood estimate for species' interaction coefficients with probability one.

## Introduction

To the extent that species interactions are important for community assembly, ecologists generally expect them to leave a signature on species' co-occurrence patterns. Using that signature to infer the underlying species interactions from observational data has been much harder, however. Disagreements about how to draw these inferences led to an acrimonious, decade-long argument among community ecologists (Lewin 1983), where essentially all of the proposed statistical approaches were criticized for having high error rates, a poor match with the underlying ecological questions, computational infeasibility, or all three (Connor and Simberloff 1979; Gilpin and Diamond 1982; Strong et al. 1984; Hastings 1987). As documented below, ecologists have, for the most part, not solved these problems in the ensuing decades. Resolving these issues would solve a longstanding issue in community ecology and make a significant contribution to other fields, such as species distribution modeling (Kissling et al. 2012).

During the time that ecologists have struggled to identify the interactions among dozens of species, bioinformaticians have largely solved the analogous problem of estimating interactions among thousands of genes from their co-expression levels (e.g. Friedman, Hastie, and Tibshirani (2008)). The discrepancy is due to the fact that ecologists have chosen to focus, almost exclusively, on overall co-occurrence rates (Connor and Simberloff 1979; Gotelli and Ulrich 2009; Gilpin and Diamond 1982; Veech 2013) or on closely-related values such as correlation coefficients (Pollock et al. 2014; see Faisal et al. 2010 and Harris 2015 for two recent exceptions). As ecologists know, however, the correlation between two

species will often reflect other factors beyond their direct pairwise interactions (e.g. abiotic influences and indirect biotic effects; Figure 1). When these factors are not accounted for, this reliance on overall co-occurrence rates can reliably lead to incorrect inferences (D. J. Harris 2015). While some methods have been proposed for incorporating a small number of specific factors (such as geographic or environmental dissimilarity) into ecologists’ null models at a time (Lessard et al. 2011), we still lack a good way to scale these approaches up for cases with many biotic and abiotic factors acting simultaneously.

A number of procedures have been developed for controlling for the influence of extraneous factors and focusing on the direct relationship between a single pair of variables, i.e. for estimating the conditional relationship between them. The most familiar of these is the partial correlation. Rather than describing the overall relationship between two variables across all conditions, partial correlations (like regression coefficients) describe the portion of the relationship that remains after the other variables in the data have been accounted for. D. J. Harris (2015) found that the partial correlation can do extract accurate information about pairwise species interactions from binary co-occurrence data in some circumstances, but the fact that this approach assumes multivariate Gaussian data makes it less appealing.

Recently, several papers have suggested that ecologists could use Markov networks (undirected graphical models also known as Markov random fields) to estimate conditional relationships from binary data by maximum entropy or maximum likelihood (Azaele et al. (2010); D. J. Harris (2015)). A Markov network defines a probability distribution over possible binary species assemblages, and its coefficients (including one coefficient describing the conditional relationship between each pair of species in the network). This approach is optimal in the sense that it produces a model that matches the observed properties of the data (i.e. the occurrence and co-occurrence rates), and that it does so with the fewest possible parameters or constraints (i.e. the Markov network has the most information entropy of any possible model satisfying its constraints; Azaele et al. 2010). As shown in D. J. Harris (2015), Markov networks do a better job of estimating species’ influences on one another better than a number of existing methods, particularly when sample sizes are low.

Unfortunately, Markov networks have an intractable likelihood function whose computational difficulty more than doubles each time a new species is added to the model. This exponential growth in the likelihood function’s complexity means that the methods that worked for Azaele et al. (2010) and D. J. Harris (2015) with networks of 20 species would be completely infeasible for networks with 50 species, requiring over a billion times more computational effort ( $2^{50}/2^{20} \approx 10^9$ ). Extending the method to account for abiotic variation among sites on the landscape would require repeating these expensive computations independently for every site, increasing the computational burden even further. If ecologists want to apply these methods to larger problems, a different model-fitting algorithm would be needed.

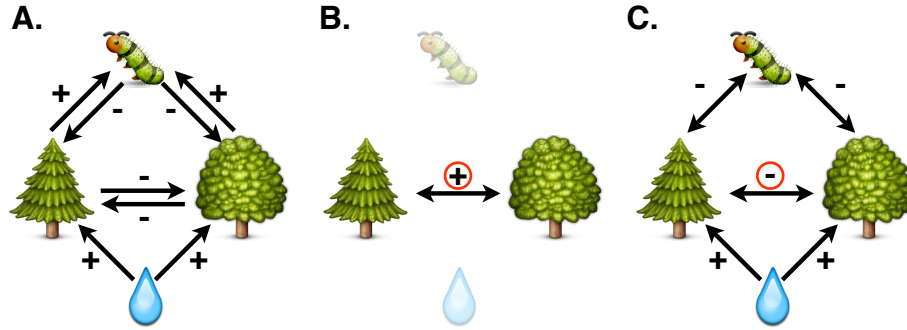


Figure 1: A hypothetical network of three species, two of which depend on an abiotic factor (annual rainfall). **A.** The “true” network involves the caterpillar exploiting the two tree species as well as competition between the two trees. The two trees also benefit from rainfall. **B.** Although the two trees directly reduce one another’s occurrence probabilities via competition, they tend to occur in the same areas (with sufficient water and without too many herbivores). An analysis that ignores these other factors could mistakenly conclude that the two trees were mutualists because of their high co-occurrence rate (circled “+” sign). **C.** The methods presented here are designed to estimate the direct interactions between each pair of species, after accounting for other species and abiotic factors that could affect their co-occurrence rates (note that the circled interaction between the trees has the correct sign). Note that, with observational data, the bi-directional effects of species interactions (pairs of arrows between species) need to be collapsed to a single number describing the conditional relationship between species (one double-headed arrow).

In this paper, I present a different way of optimizing the likelihood, called “stochastic approximation” (Robbins and Monro 1951; Salakhutdinov and Hinton 2012), which replaces the intractable computations with tractable Monte Carlo estimates of the same quantities. Despite the sampling error introduced by this substitution, stochastic approximation provides strong guarantees for eventual convergence to the maximum likelihood estimate (Younes 1999; Salakhutdinov and Hinton 2012). This change in approach makes it feasible to estimate the interactions among hundreds of species from observational data while also accounting for possible responses to abiotic factors (such as those used in species distribution models), giving ecologists some power to distinguish between species pairs that co-occur due to shared environmental tolerances from those that co-occur due to direct interactions like mutualism.

## Methods

### Markov networks

As discussed in Azalee et al. (2010) and D. J. Harris (2015), Markov networks such as the Ising model (Cipra 1987) can be used to describe community structure as follows. Each species is represented by a binary random variable, describing whether it is present (1) or absent (0). A species’ conditional probability of presence under a given set of biotic and abiotic conditions depends on its coefficients. The coefficients linking species to one another describe their conditional associations: all else equal, a species will occur less often in the presence of its competitors and other species with which it is negatively associated, and more often in the presence of its mutualists:

$$p(y_i | \vec{y}_{j \neq i}) = \text{logistic} \left( \alpha_i + \sum_{j \neq i} \beta_{ij} y_j \right),$$

where  $y_i$  is 1 when species  $i$  is present and 0 when it is absent,  $\alpha_i$  is an intercept term,  $\beta_{ij}$  represents the conditional relationship between species  $i$  and species  $j$ , and  $\text{logistic}(x) = e^x / (1 + e^x)$ . These conditional probabilities can be combined to calculate the probability of observing any given combination of presences and absences, up to a multiplicative constant (Lee and Hastie 2012; Murphy 2012):

$$p(\vec{y}) \propto \exp \left( \sum_i \alpha_i y_i + \sum_{j \neq i} \beta_{ij} y_i y_j \right).$$

Unfortunately, the exponentially large number of possible assemblages makes the normalizing constant for this joint probability distribution intractable when the number of species is larger than 20 or so. However, it is generally straightforward to simulate examples of assemblages that are consistent with graphical models

such as these, using Monte Carlo techniques like Gibbs sampling (Salakhutdinov and Hinton 2012). Gibbs sampling is especially convenient for these models because it only requires the conditional probabilities, which are straightforward to compute (Harris 2015; Appendix).

In each of the scenarios below, the “observed” landscapes were simulated using Gibbs sampling from a pre-specified set of “true” parameters, then stochastic approximation was used to recover these parameters from the simulated presence-absence data.

## Conditioning the network on the abiotic environment

The Markov networks fit in D. J. Harris (2015) treated the  $\alpha_i$  terms from Equations 1 and 2 as constants, meaning that the models expected each species to have the same conditional occurrence probability in any location with a given set of facilitators and competitors. In this paper, I extend the model so that the local abiotic conditions can also affect species occurrence probabilities directly. Specifically, the  $\alpha_i$  terms in these analyses are linear combinations of the local environmental conditions, represented by  $x_1$  through  $x_5$ . By estimating the coefficients associated with each of these  $x$  variables for each species, we can account for their responses to the abiotic environment as well as to one another. In other fields, a model like this one, where a Markov network’s parameters depend on external factors is called a conditional random field (Lee and Hastie 2012); these models have been used in a variety of contexts, from language models to image processing (Murphy 2012).

## Coefficient estimation with stochastic approximation

A Markov network describes a probability distribution over possible assemblages. Since the model is a member of the exponential family it can be summarized without loss of information by its “sufficient statistics”. For the model presented here, the sufficient statistics include: the number of occurrences for each species, the number of co-occurrences between each species, and the cross-product between the species and environment matrices (Azaele et al. 2010; Lee and Hastie 2012; Murphy 2012). Finding the maximum likelihood estimate for the model parameters is equivalent to minimizing the discrepancy between the values of the data’s sufficient statistics and the expected sufficient statistics under the model (Bickel and Doksum 1977). Because fully-observed Markov networks, such as the ones analyzed here, have unimodal likelihood functions (Murphy 2012), it is possible to find the global optimum by iteratively reducing the discrepancies between the sufficient statistics of the model and of the data to zero.

In order to reduce the discrepancy between the observed and predicted sufficient statistics, the **rosalia** calculates each value exactly, averaging over all possible presence-absence combinations. Stochastic approximation (Robbins and Monro

1951; Salakhutdinov and Hinton 2012) instead estimates the expected values of the sufficient statistics by averaging over a more manageable number of simulated assemblages during each model-fitting iteration, while still retaining maximum likelihood convergence guarantees. The procedure iterates through the following three steps as many times as needed (50,000 for these analyses; see Appendix for annotated R code):

- 1: simulate a set of assemblages from the current model parameters and calculate sufficient statistics for the sample.
- 2: subtract the simulated sufficient statistics from the observed ones to calculate the approximate likelihood gradient
- 3: Adjust the model parameters to climb the approximate gradient, using a schedule of step sizes that satisfies the criteria in Chapter 6 of Powell (2007).

Here, the simulations in Step 1 used Gibbs sampling to generate examples of landscapes based on the model’s current parameter estimates. While the simulated landscapes produced by Gibbs sampling are serially autocorrelated, statisticians have shown that this merely slows convergence to the maximum likelihood estimate rather than preventing it altogether (Younes 1999; Salakhutdinov and Hinton 2012).

The approximate likelihood gradients in Step 2 match the ones from D. J. Harris (2015), except that they are averaged over a set of Monte Carlo samples rather than over all possible presence-absence combinations. These gradients were augmented with a momentum term (Hinton 2012) and by regularizers based on a logistic prior with location 0 and scale 2.0 (for environmental responses) or 0.5 (for pairwise interactions).

The step size parameter in Step 3,  $\alpha_t$ , decreased after each iteration according to a generalized harmonic sequence,  $\alpha_t = \alpha_0 1000 / (999 + t)$ , which satisfies the criteria in Powell (2007). The scaling factor,  $\alpha_0$ , was 1.0 for species’ intercepts and environmental responses. Because of the enormous number of pairwise interaction coefficients, I set  $\alpha_0$  to 0.1 for the  $\beta$  parameters.

## Simulated landscapes with known interactions

In order to assess the models’ ability to recover the “true” parameters that generated a presence-absence matrix of interest, I first needed to generate such matrices from known processes.

To demonstrate that my stochastic approximation implementation could converge to the global optimum, I first simulated a landscape with 20 species and 500 sites, using Gibbs sampling. These landscapes had few enough species that the `rosalia` package for estimating Markov networks (David J. Harris 2015) could find the penalized maximum likelihood estimates for the Markov network in a reasonable amount of time. For each of these simulated landscapes, I then fit

the same Markov network model to the simulated data using the exact approach from D. J. Harris (2015) and the stochastic approximation method described above.

I then simulated a large landscape with 250 species and 2500 sites, representing a large data set roughly the size of the North American Breeding Bird Survey. Each site on the landscape was represented by 5 environmental variables, which were drawn independently from Gaussian distributions with mean 0 and standard deviation 2.5.

Each species was assigned two sets of coefficients. The coefficients determining species' responses to the environment were each drawn from standard normal distributions. The coefficients describing species' pairwise interactions were drawn from a mixture of normals (see Appendix) so that most interactions were weak and negative, but a few strong positive and interactions also occurred.

The coefficients described above are sufficient to define each species' conditional occurrence probability (i.e. its probability of occurrence against any given backdrop of biotic and abiotic features). I used these conditional probabilities to produce examples of communities that were consistent with the competition parameters and with the local environmental variables via Markov chain Monte Carlo (specifically, 1000 rounds of Gibbs sampling; see code in the Appendix). I then used the methods from the next section to attempt to infer the underlying parameters from the simulated data.

## Results

For the smaller communities, the squared deviations between the exact estimates produced by the `rosalia` package and the ones produced by stochastic approximation quickly decayed to negligible levels (Figure 2A), indicating that the stochastic approximation procedure was implemented correctly and worked as the mathematical theory predicts.

For the larger landscape, I found that the stochastic approximation approach achieved reasonably good performance after ten minutes of optimization (Figure 2B). After 50,000 iterations (about 5.4 hours on my laptop), the model was able to recover more than two thirds of the variance in species' pairwise interactions ( $R^2 = 0.71$ ; Figure 3A), and nearly all of the variance in their responses to environmental variables ( $R^2 = 0.95$ ; Figure 3B).

## Discussion

For decades, ecologists have relied on poor test statistics for inferring species interactions from observational data (D. J. Harris 2015). As shown here and in D. J. Harris (2015), however, these inferences can only be made reliably by

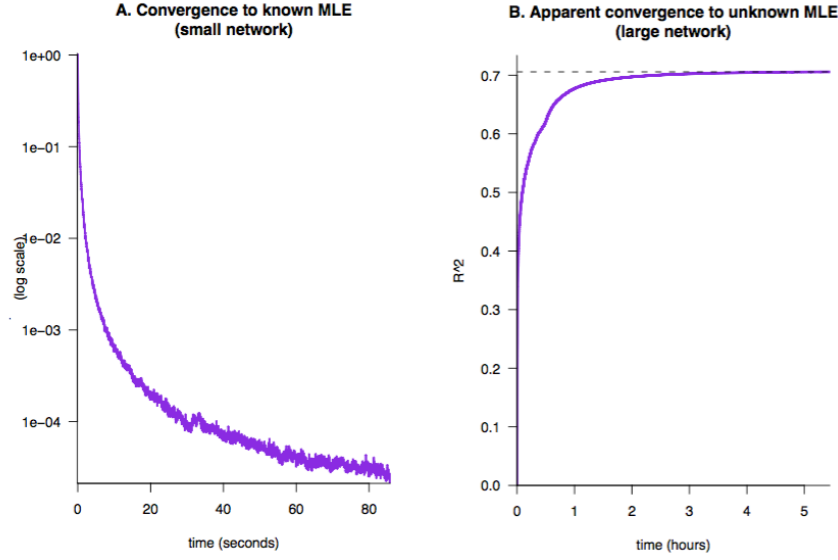


Figure 2: Stochastic approximation improves the model over time. **A.** With small networks where the exact maximum likelihood estimates are known, stochastic approximation approaches the global optimum very quickly (note the log scale of the y axis). Within a few seconds, the mean squared deviation between the approximate and exact estimates drops to less than 0.01; in less than a minute, it drops below 0.0001. For comparison, the `rosalia` package took about six minutes to find the maximum likelihood estimate. **B.** With larger networks, where the maximum likelihood estimate cannot be calculated exactly, stochastic approximation converges to an apparent optimum that explains most (but not all) of the variation in the “true” parameter values.



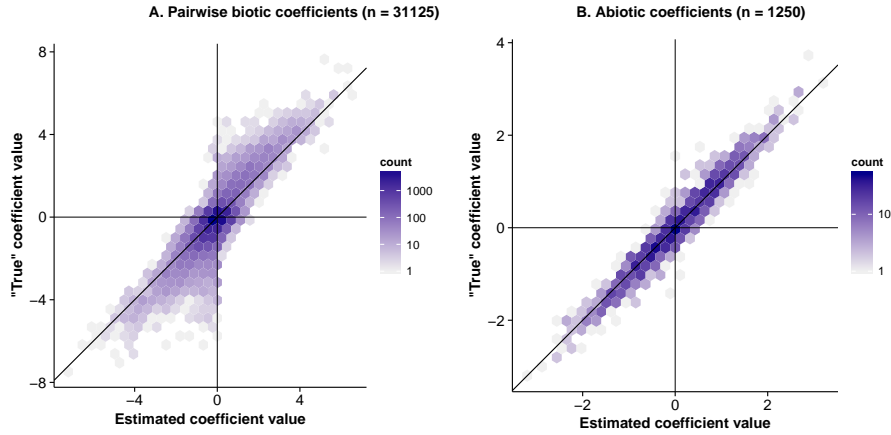


Figure 3: “True” versus estimated network parameters for all 250 species’ responses to the other 249 species in the data set (**A.**  $R^2 = .71$ ) and to the 5 abiotic variables (**B.**  $R^2 = .95$ ).

methods that control for other species in the network, such as partial correlations or Markov networks. The biggest computational problem with large Markov networks is the impossibility of averaging over all their possible states, but these results demonstrate that this step can be avoided in ecological analyses. Stochastic approximation is able to recover the same estimates as exact methods for smaller networks, while scaling gracefully to networks with hundreds of species.

The largest downside of using stochastic approximation instead of the exact methods introduced in D. J. Harris (2015) is the difficulty in generating confidence intervals. The `rosalia` package can produce confidence intervals based on the Hessian matrix, but it is not feasible to calculate this matrix for large networks. It may turn out that the best way to generate confidence intervals for large networks is by repeatedly fitting the model to bootstrapped samples of the data. Alternatively, ecologists may be able to take advantage of the advanced Monte Carlo techniques introduced in Murray, Ghahramani, and MacKay (2012) to sample from the posterior distribution over possible parameter values, which could be used to generate credible intervals for the parameter estimates. Other advanced Monte Carlo methods (e.g. Salakhutdinov 2009) may also speed up convergence to the maximum likelihood estimate in cases where serial autocorrelation in the Gibbs sampler is too strong for effectively sampling the space of possible landscapes.

As the number of potentially-interacting species increases, the number of adjustable parameters increases even faster, so overfitting becomes a major concern. Fortunately, a number of good regularizers have been proposed. Of these, some of the most interesting options include  $L_1$  regularization, which ensures that

many of the estimated coefficients are exactly zero (Lee and Hastie 2012). This sparsity matches ecologists’ intuition that many species from different guilds are unlikely to interact much at all (Faisal et al. 2010), and also produces computational benefits for model estimation. Of course, the best regularizers will take advantage of specific ecological knowledge (e.g. from field experiments, natural history, or trait data) to provide information about individual pairwise interactions, rather than about their overall distribution.

These richer sources of information will be especially important for cases where ecologists expect that the interactions between species are asymmetric (e.g. where only one species is affected by an interaction or where one species benefits at a cost to the other). With snapshot observations of species’ spatial associations, as discussed here, interactions must be reduced to a single number describing the net association, as in undirected models such as the Markov networks presented here (Schmidt and Murphy 2012). With richer data types, however, ecologists could more easily learn about asymmetric interactions such as facilitation, predation, and parasitism.

Even without better data, ecologists have a number of options for expanding beyond simple Markov networks in a number of ways that would improve their ability to address a wider range of questions. This paper demonstrated that it is possible to simultaneously estimate species’ responses to the abiotic and environment and to one another, but many other extensions are possible. For example, ecologists could condition the model on variables whose values have not been measured (e.g. partially-observed Markov networks, or the approximate networks in the `mistnet` package; cf. Pollock et al. (2014)). This would allow ecologists to account for measurement error and for other ecologically-important factors that can be difficult to measure. Ecologists should also explore higher-order networks, where one species’ presence can affect the relationship between two other species (Whittam and Siegel-Causey 1981; Tjelmeland and Besag 1998).

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