Predicting biodiversity dynamics in response to environmental change

Can we do it? A report from assess.sim.basic.R

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Abstract

"Lorem ipsum dolor sit amet, consectetur adipisicing elit, sed do eiusmod tempor incididunt ut labore et dolore magna aliqua. Ut enimad minim veniam, quis nostrud exercitation ullamco laboris nisi ut aliquip ex ea commodo consequat. Duis aute irure dolor in reprehenderit in voluptate velit esse cillum dolore eu fugiat nulla pariatur. Excepteur sint occaecat cupidatat non proident, sunt in culpa qui officia deserunt mollit anim id est laborum."

Contents

Introduction

Overview

As water temperatures change, species may shift the size and location of their geographical ranges, bearing consequences for the food webs and economies linked to those species. However, species don't always respond similarly to shifting temperatures (different thermal tolerances, e.g.), which means that changing temperature may remix the composition and diversity of ecological communities.

The biological, spatial, and temporal scale of community diversity shifting in response to climate is massive. A functional definition of a community may consist of 100's or 1000's of species, each of which may be shifting its range at a scale of decades and 100's kilometers. As a result, we need statistical methods for estimating biodiversity that don't rely on heavy replication and that make efficient use of available data. Enter the superstars: on the data side the trawl data set has amazing spatiotemporal and taxonomic extent and resolution; on the statistical side multispecies occupancy models (MSOM) are hierarchical state space models that are designed to estimate species richness and don't require consistent or extensive "replication". Although they're superstars, even these data and models have their limitations and pitfalls.

Can we estimate the dynamics of species richness from trawl data using an MSOM? It's a hard question to answer because we can never know the "truth" for sure, but we can get an idea of how reliable our analysis is by simulating fake data, for which we know true values because we created them. The trawl data set is generated by two distinct processes: Nature's data generating process (NDGP), and the process by which humans observe the result of NDGP. So we ask: to what extent is the accuracy of estimates from an MSOM dependent on characteristics of NDGP, and in particular, the way in which we observe the result of NDGP? The strategy for answering this question is to simulate fake data where we approximate Nature but gain knowledge of "truth", "observe" the results of the true process, then try to recover the true species richness from these simulated data.

The Simulation

The goal of this simulation was to use a very basic process to generate presences and absences of species in space and time. In this version of the simulation, there is no explicit connection between years (they are independent). There is a modest spatial connection, because in the simulation an environmental variable determines habitat suitability. I think of this environmental variable as temperature, and I filled a grid with temperatures that ranged from the coldest at the top of the grid (north) and the warmest at the bottom (south) and added random variation among columns in the same row (among longitudes at the same latitude).

One level of the simulation mimics NDGP. In this level, NDGP is best characterized by ψ, which is the product of a temperature and species' response curves. I.e., temperatures were used to determine the suitability of each grid cell to each simulated species. This suitability is known as ψ throughout this document.

A second level of the simulation mimics human observation of NDGP — what we do when we collect data. This process was simulated by assigning each species has a unique probability of being observed or "detected" (this variable is p). The observation process gets several attempts at observing a given species in a given grid cell; think of this as subdividing each site into subsites, and when you visit each subsite you have probability

p of observing a particular species (each species has its own p). Depending on the settings used in the analysis that this document summarizes, the maximum number of subsites can vary, as can the number of subsites per site (OK, fine; the maximum number of subsites in this version is 4, the number of subsites per site varied between 1 and 4, and overall 50% of total possible subsites were sampled).

As previously mentioned, the simulation included "time". In this basic version, not much changes between the "years" for the true process (temperature doesn't change, nor do the response curves), but the mean of p does change. In a given year, the entire community has an overall mean probability of being detected, and each species randomly deviates from that mean.

The simulation also has replicates. To understand the replicates, it needs to be clear that even when a parameter in the simulation does not change, the outcome can change. The replicates hold the realization of the simulated NDGP constant, and draw new realizations of the observation process. I.e., both ψ and p are constant among replicates, and the binary *outcome* of ψ is also held constant, but the outcome for p can change. Furthermore, although each replicate has same values of p (both the mean p and each species' individualized random draw from that distribution), each replicate switches which year is associated with which p's. In this way we can observe each outcome of Nature's data generating process under a series of settings for the human observation process.

Multispecies Occupancy Models (MSOMs)

Multispecies occupancy models are Bayesian statespace hierarchical models. They distinguish between truth and observation of the truth, and many parameters share a common "parent" distribution. They are very flexible models, and can be adapted to include new types of processes. The MSOM being used here is a relatively simple version of these models. It predicts the probability of each species existing in a grid cell from a logistic regression equation that uses a second-order polynomial of the environmental variable as a covariate. The parameters in this level of the model are hierarchical, with species having their own paramter values, but these individual parameters are not wholly independent in the sense that they share a common parent distribution, which sort of acts to both limit how different they can be and to inform one another. The model also has an observation level, which only has a hierarchical intercept (just a mean) as a predictor variable.

The MSOM makes guesses of the true state of the system (whether a species is actually present or not). It then makes guesses at how the observation of that true state might turn out, which is effectively a prediction of what our data will be. The Bayesian model fitting process then uses this comparison of the observed data to the estimate of the observation to tweak the parameters in the MSOM. This process is repeated until the choice of paramters boils down to what is essentially the posterior distribution of the estimated parameters.

Right now the MSOM model is fit separately to each year and each replicate. So the model never gets to see multiple years or multiple replicates at the same time. Furthermore, when referring to a parameter value fitted in the MSOM, it is implied that it can be subscripted with time or replicate (because all years and replicates are fit independently).

The parameters in the logistic regression that predicts the value of ψ vary among species, although *psi* itself varies among species and space, because the regression parameters (subscripted by species) are multiplied by the environmental variable (subscripted by space). More or less, it can be said that, for a given species, ψ

varies among space because of the environmental variable, and in a given location it varies among species because of the regression parameters.

Conventions and Settings

In this section I outline the subscripting and notation used in the MSOM analysis and for the simulation. I also outline various settings (number of species simulated, replicates, etc.). Most of the numbers you see (and some of the text) is dynamically generated based on the code that produced the statistics and figures. Therefore, you can refer back to these sections to see what settings may have changed since the last version of this document.

Note: *I've often found myself having to get creative with subscripts and superscripts. I've tried to be clear an consistent, but small inconsistencies likely exist, so don't be confused by them. For example, if you see* $max(Z)$ *and* Z_{max} *in two different sections, they are probably referring to the same thing. If you see something confusing, let me know (preferably by (creating an issue on GitHub)[https://github.com/rBatt/trawl/issues]), and I'll fix it.*

Dimension Conventions

Summary

1. Site ($j = 1, 2, \ldots, j_{max} = 9 \times 9 = 81$)
    - Sites are unique combinations of latitude and longitude
    - The spatial arrangement of sites is *not* arbitrary, although importance depends on settings (see `dynamic` below)
    - The environmental variable X varies among sites (and years, below)
2. Sub-sites ($k = 1, 2, ...$)
    - Sub-sites are only relevant to the "observation" process
    - Each site has the same number of possible sub-sites, but the number of sub-sites observed can vary
    - In this simulation, $k_{max} = 4$, $k_{min}^{observed} = 1$, and $k_{max}^{observed} = 4$
    - Substrata are are primarily useful for determining p, the detection probability
3. Species ($i = 1, 2, \ldots i_{max} = R = 30$)
    - Does not include "augmented" species
    - For this MSOM analysis, the species array was padded with 10 0's
4. Time ($t = 1, 2, \ldots 4$)
    - Time is primarily used to vary the parameters controlling the "true" process
    - When those parameters don't change, time provides independent*realizations of the same "true" process
        - **Note: only when* `dynamic=FALSE` *in* `sim.spp.proc`

5. Replicates ($r = 4$)

   - Replicates are *simulated* repeated human observations of the same *realization* of the "true" process at Time_t
   - Replicates are used to vary the parameters that control the "observation" process
   - When those parameters don't change, each replicate provides an independent*realization of the same "observation" process

In Code

The MSOM analyzes each year_t–replicate_r combination independently. Parameters subscripted by these dimensions are derived from separate analyses.

In my code, I've tried to be consistent in my use of these indices to describe arrays, matrices, and rasters. Rows are dimension 1, columns dimension 2, etc. The precedent of subscripted dimensions follows the numeric ordering of the list above. E.g., in the matrix $X_{i,t}$ each row will refer to a different species, and each column a different year (note that site_j is skipped, so species_i is "promoted" to dimension 1, the row.). By default, R fills matrices and arrays by column, whereas the `raster` package fills them by row. In most cases where an R object needs to split sites into the lat/ lot components, I make use of the `raster` package. Therefore, the numbering of the sites proceeds row-wise, where each site is numbered according to the order in which it is filled, as in this 2×3 matrix: $J = \begin{pmatrix} 1 & 2 & 3 \\ 4 & 5 & 6 \end{pmatrix}$

Note that even though this matrix is numbered row-wise, it is still indexed as $J_{row,column}$, such that $J_{1,2} = 2$. As mentioned previously, this information is primarily important for understanding the code involved with this project, and in most cases it is not crucial to be explicitly aware of the spatial arrangement of sites.

Settings

Simulation Settings

I created a class called `"spp"`, which has methods for `print()`. The `Dimensions` are the number of sites, the number of species, then the number of years.
Also `print`ed are some richness summary statistics. `All cells` refers to the collective richness over all j taken together. The meaning of `One cell` differs slightly between the true and observed printouts: in the true printout the richness is of a particular site (j), and in the observed printout it is of a particular sub-site (k).

```
## Dimensions: 81, 30, 4
## grid.h = 9
## grid.w = 9
## grid.t = 4
##
## Number Species Possible (ns):
```

```
## 30
## Total Species Richness:
## 30
## Total Observed Species Richness:
## 30
##
## Annual Species Richness:
##           Min. 1st Qu. Median  Mean 3rd Qu. Max.
## All cells   29      29     29 29.25   29.25   30
## One cell     5      10     14 13.63   17.00   24
##
##
## Observed Annual Species Richness:
##           Min. 1st Qu. Median   Mean 3rd Qu. Max.
## All cells   27   27.75   28.5 28.250      29   29
## One cell     0    0.00    0.0  4.008       7   23
```

In the MSOM, detectability (p_i) is determined in the form of a logistic regression, which currently only has an intercept (v_0) as predictor (so just a mean). That intercept varies among species (i.e., $v_{0,i}$), and that variation is generated by drawing each individual species's intercept ($v_{0,i}$) from a parent distribution: $v_{0,i} \sim \mathcal{N}(\mu_{v_0}, \sigma^2_{v_0})$. See section about p for more info.

year	mu.v0	sigma.v0
1	-2	2
2	0	2
3	2	2
4	4	2

Settings for JAGS & MSOM

nChains	nIter	n0s	nSamples
3	50000	10	500

In the table above, `nChains`, `nIter`, and `nSamples` are all variables that are strictly pertinent to the Bayesian analysis carried out in JAGS. The `n0s` value refers to the the degree of "data augmentation". In this process, you add extra species to the data set, and say that they were never observed. For our purposes, this is employed for purely technical reasons, although it can be used to extra further inferences about species richness.

The posterior samples from JAGS consist of 500 samples (above). However, to save memory and hard drive

space, I have often only saved measures of central tendency for each of these. In this assessment, I have performed all calculations on the `centralT`=**median** of the posterior samples.

Species Richness

Definition of species richness

Species richness is the number of different species, or more generically, unique taxa. The point is moot in the simulation study, and in the empirical trawl data it refers to species.

Estimates of richness (R) can be made spatially or temporally explicit (or neither, or both). In the following figures, different levels of aggregation are performed – for most figures R is split by year (this is true for all figures but the Boxplot Figure). The Time Series of Richness Figure emphasizes temporal dynamics and keeps replicates separated, but aggregates over space (the j sites). The `Nsite` Scatter Figure doesn't aggregate over space or time, but it does aggregate over "replicate" observations; importantly, while the figure does present any spatial aggregation, it does not retain the spatial relationship (you can't tell which sites are next to others). The final two figures of the section (Heatmap of of Richness Figure) are similar to the previous figure, except that spatial relationship among points is retained via a heatmap representation.

None of these estimates of richness include the 10 species that were part of the "data augmented"/ "adding 0's" process. Richness values can either be true (true simulated NDGP; R^{true}), observed (true simulated human observation of NDGP; R^{obs}), or MSOM estimates of one of those two ($\hat{R}^{true}$ or $\hat{R}^{obs}$).

Regional Richness

These estimates of species richness only distinguish between replicates and years. They do not contain any site-specific information.

Richness Boxplots

With the boxplots we're mostly looking to see if the estimates of richness vary with the mean probability of detection, p. In the empirical data, we know that taxonomic identification changed over time (it improved; generally, more species were ID'd in later years). We also suspect that gear might change, which affects the probability of observing a species. The "Average Detection Probability" category in the boxplots is the cross-species average of p (which with large sample size approach the hyperparameter p_μ).

Richness Time Series

Text explanation goes here

Need explanations for how each panel was calculated.

1. R^{true} is straightforward

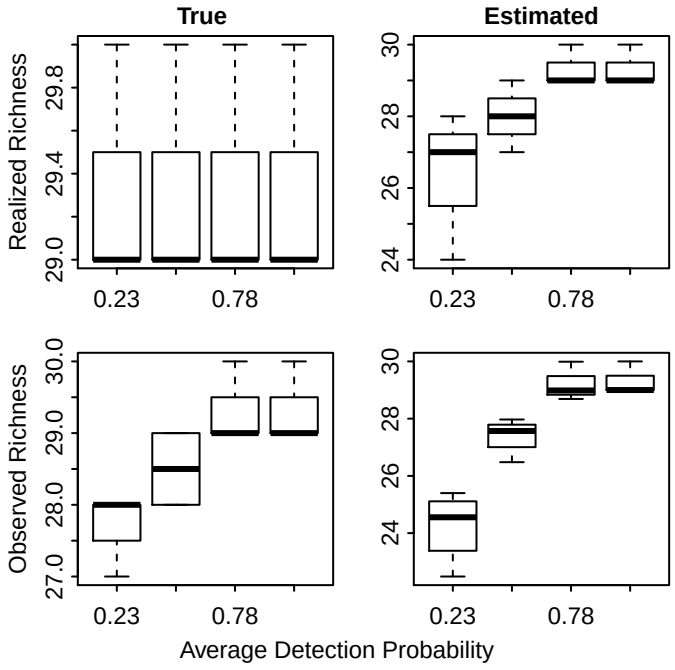

Figure 1: Boxplots of species richness. Numeric groupings indicate the average value of p across species during a given year–replicate combination. The panels in the left column are the true simulated values, and the panels on the right are the corresponding MSOM estimates. The top row indicates the latent realized species richness or MSOM estimates of the richness. The bottom row's panels are the simulated observed values of richness (the response variable in the MSOM) and the MSOM estimates of the observed values.

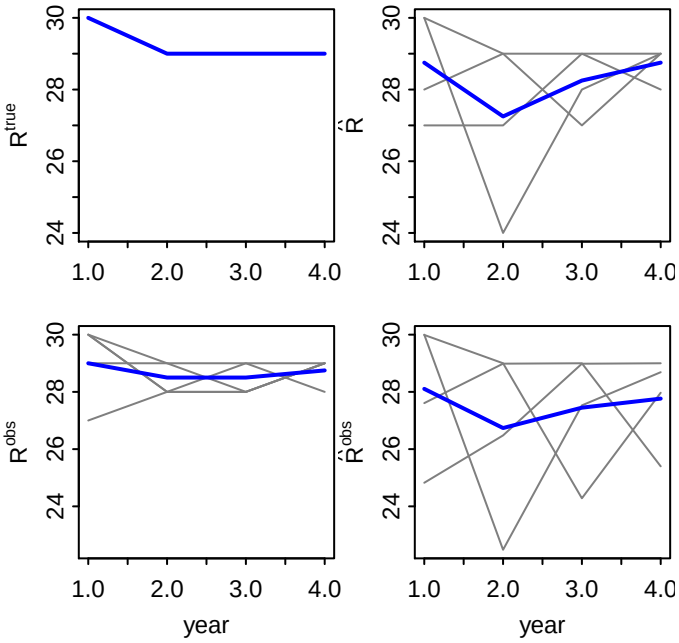

Figure 2: Time series of richness. Gray lines are individual replicates. Blue lines are averages. Note that detection probabilities ($p_{i,t,r}$, see simulation settings above, as well as definition of p below) change over time, and their temporal ordering differs among replicates.

2. $\hat{R}$ is from $\sum_{i=1}^{R^{true}} max(\hat{Z}_{i,\nabla j \in J})$; and to be clear, $\hat{R}$ does not include the "unobserved" species introduced to the MSOM occurrence matrix (Y)

Site Specific Richness (`Nsite`)

Scatter Plots of `Nsite` Split by Year

Maps of Richness (space and time)

Text explanation goes here

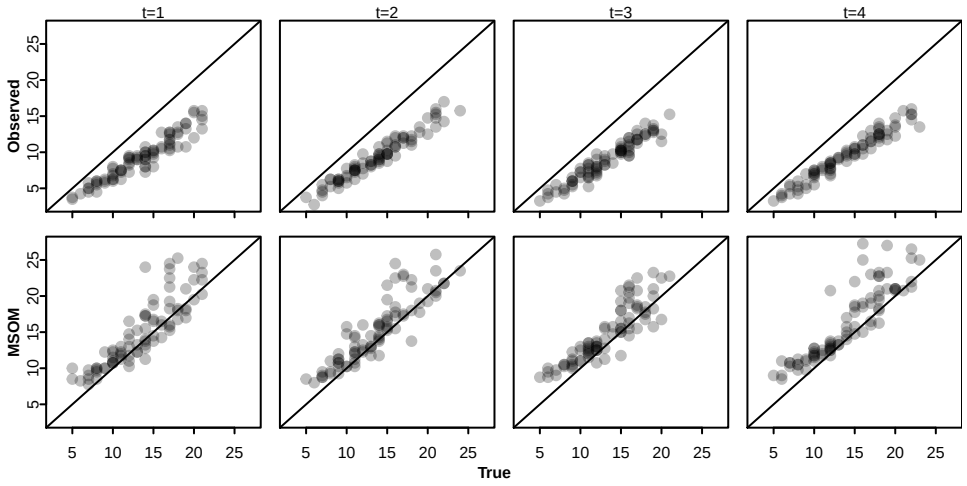

Figure 3: Site-specific richness (`Nsite`, N_j) from simulated observations (vertical axis, top row; N_j^{obs}) and from MSOM estimates (vertical axis, bottom row, $\hat{N}_j$) vs true site-specific richness (horizontal axis; N_j^*). The panel columns delineate the years of the simulation. Each point is site-specific species richness that has been averaged over the simulated replicate observations.

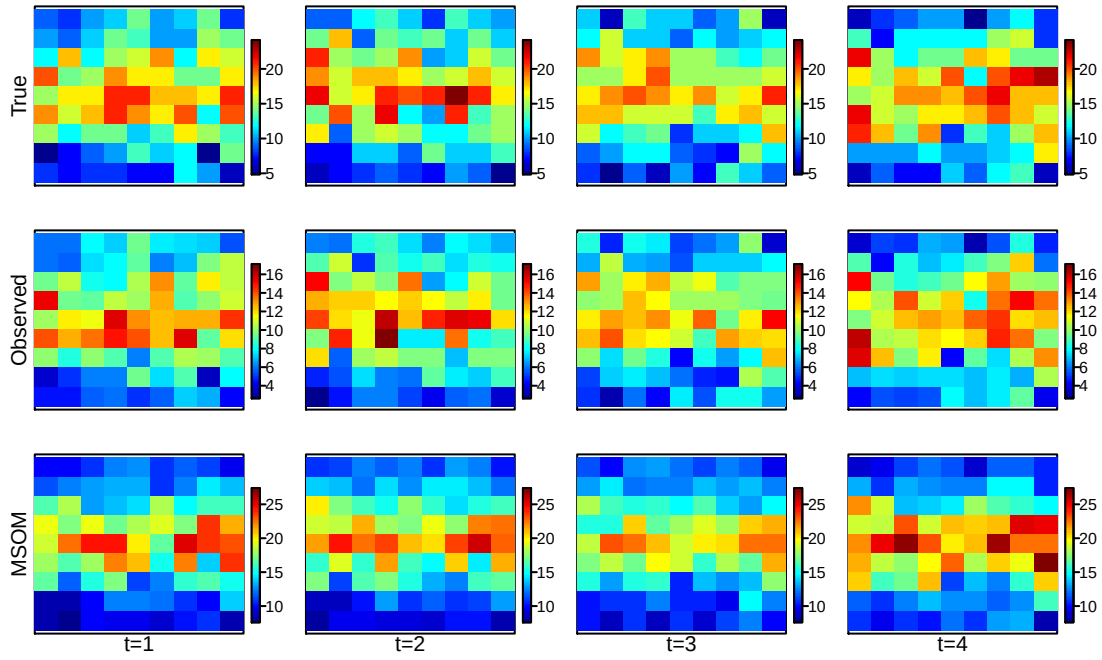

Figure 4: Maps of site- and year-specific species richness (`Nsite`) from the simulation of the True process (top row), simulation of the Observed process (middle row), and the MSOM estimates (bottom row). X-axis and Y-axis indicate position in 2 dimensional space; it is important to note that the environmental variable changes linearly across the y-axis, and randomly (and much less) across the x-axis. The different columns represent separate years. The environmental variable changes linearly among years (the rate of change is the same for all x-y locations). Colors indicate species richness (warm colors are higher richness than cool colors), averaged over the simulated replicate observations. Horizontal and vertical axes Each row of panels is scaled independently, columns within a row are scaled equally.

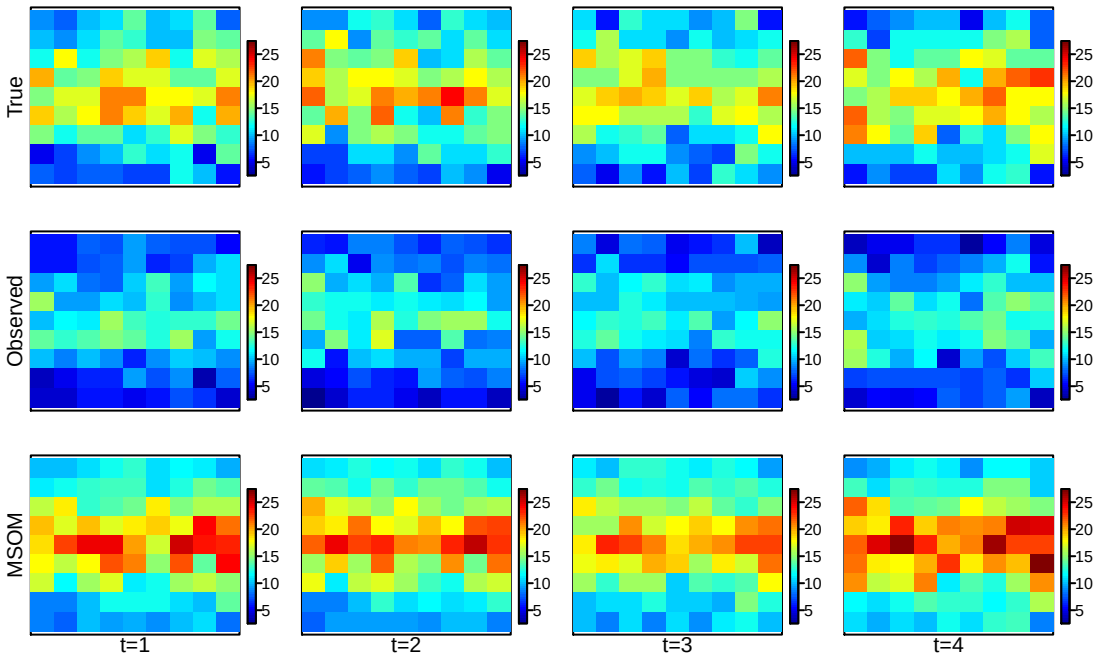

Figure 5: Same as previous figure, but all panels are on the same scale.

Occupancy Probability, ψ

Definition of ψ

Definition description goes here
Probably need to describe how it's generated in the simulation
As well as how it's estimated in the MSOM
In particular, important to point out that they may or may not match

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Scatter Plot of Aggregated ψ

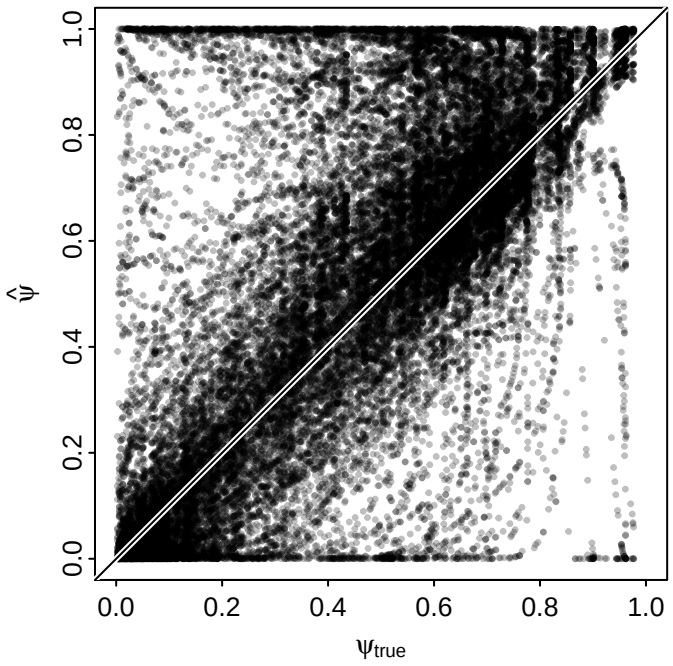

Figure 6: MSOM estimates of ψ ($\hat{\psi}$) vs. true values of ψ (ψ_{true}). Each point is a ψ value for a particular site-species-year-replicate. The white and black line is the 1:1 line.

In a general sense, the MSOM can distinguish between instances (sites/ years) when a species is likely to be present, and when it's not. However, in every simulation I've done (varying many parameters that aren't compared in this document), the scatter plot of ψ always makes it apparent that

1. There is a lot of variability around the 1:1 line

2. The residuals are not normal, and they are not independent
    i. In general, I've found that $\hat{\psi}$ exhibits an upward bias, overestimating ψ^{true}

ii. Smoothly-curving excursions from the 1:1 line often prominent

These patterns are somewhat concerning. The curve-like sequence of residuals is probably a byproduct of slightly incorrect estimates of the parameters in the logistic regression ($[a_0, a_1, a_2]$), resulting in estimated response curves that deviate non-randomly from the true response curve. For a heuristic of how these smoothe excursions can occur, in R try something as simply as `d <- rnorm(100); plot(dnorm(d), dt(d, 1))` to see the relationship between the density estimate from the correct distribution and that from the wrong distrubtion (the density is analogous to ψ); or for really crazy patterns, try `d <- rnorm(100); plot(dnorm(d), do.call(approxfun, density(d)[c("x","y")])(d))`. So the curves are explainable, but I cannot explain the consistent overestimation; I could understand how underestimating detectability (p) would result in overestimating ψ, but the MSOM appears to recover true p values rather well (e.g., see p Scatter Figure), so that's not a satistfying explanation.

In the next section I drill into ψ a bit more to try and understand what causes the largest deviations from true values.

Scatter Plot of $\hat{\psi}$ vs ψ_{true}, split by year and replicate

The estimates and true values of ψ are best correlated when p is high. When the average species has a low chance of being detected (when p_μ is, say, 20%), the estimates of ψ are a mess.

Note: what I refer to as p here is really just the probability that a species will be detected if an occupied site is sampled, so the number of substrata sampled per site isn't relfected in p. In this simulation, 50% of substrata were sampled, and while this doesn't influence p, it could add noise to its estimates.

Occupancy Response Curves

Occupancy response curves are calculated as $logit(\psi_i) = \mathbf{X} \times \mathbf{a_i}$, where

$$\mathbf{X} = \begin{pmatrix} 1 & X_{min} & X_{min}^2 \\ \vdots & \vdots & \vdots \\ 1 & X_{max} & X_{min}^2 \end{pmatrix}; \mathbf{a_i} = \begin{pmatrix} a_{0,i} \\ a_{3,i} \\ a_{4,i} \end{pmatrix}$$

Therefore, these curves are tantamount to values of ψ, except that ψ generally pertains to a simulated, observed, or true occupancy probability, whereas the occupancy probability in the response curves is calculated over hypothetical conditions (i.e., over hypothetical values of the environmental gradient X).

True Occupancy Response Curves

In the response curve, the values of the environmental variable are an arbitrary gradient, and do not necessarily correspond to what was observed in the simulated environment (although they are intended to cover the same range).

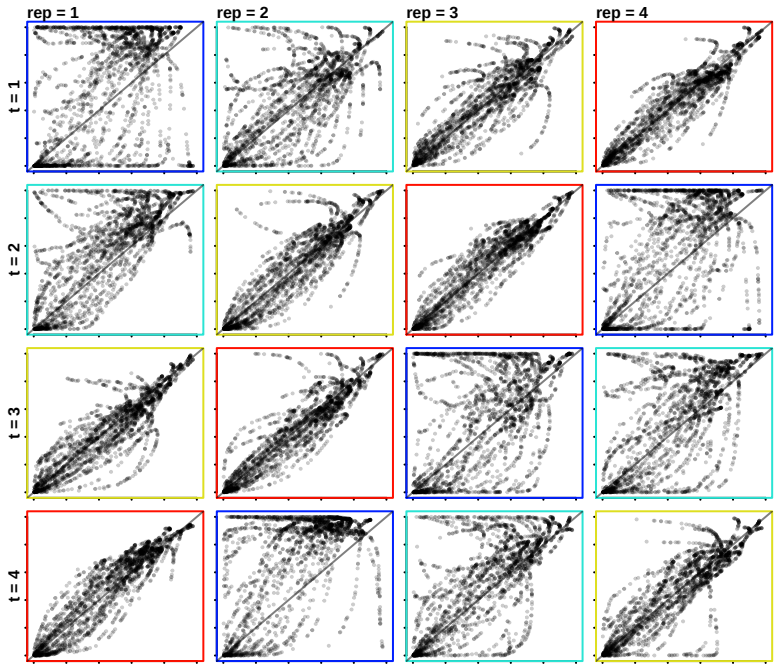

Figure 7: True (horizontal axes) and MSOM estimates (vertical axes) of occupancy probabilities ($\psi_{j,i,t,r}$) of species i occupying a location j. Years (t) are separated by rows, replicates (r) are separated by columns. The border color of each panel indicates the community-level mean probability of detection (p_μ; where $p_i \sim \mathcal{N}(p_\mu, \sigma^2)$), with warm colors indicating high detectability, and cool colors low. The species-specific detectabilities are **not** re-randomized among replicates, but even when the probabilities associated with the observation process do not change, the outcome of the process can change. The year t of the simulated true process changes across the rows of panels, and the simulated replicate observation r changes across columns.

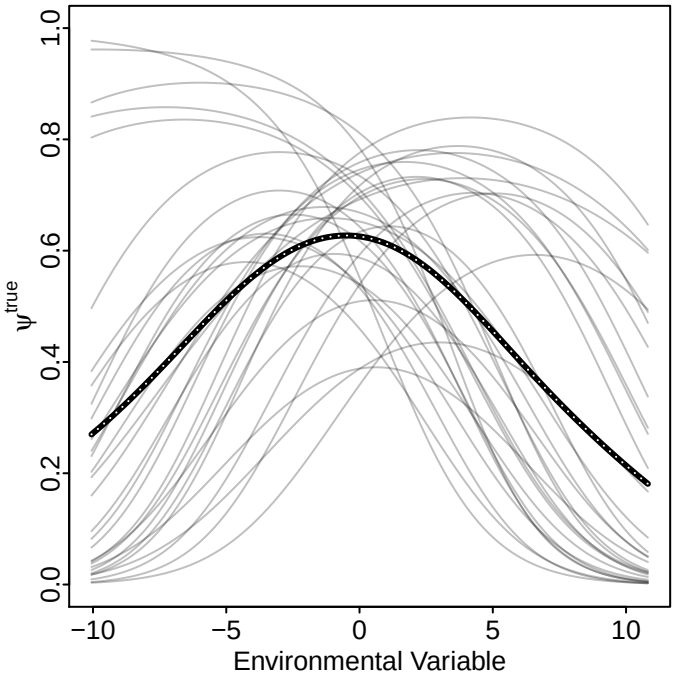

Figure 8: True simulated response curves. Vertical axis is the value of ψ^{true}, horizontal axis is the value of the environmental variable that, along with species-specific regression parameters, determines ψ^{true}. The thick line is the among-species mean value of ψ^{true} at a given value of the environmental variable.

Estimated Occupancy Response Curves

($min(X) = -10.1$, and $max(X) = 10.8$)

(red; $p_{max} = 0.93$)

(blue; $p_{min} = 0.23$)

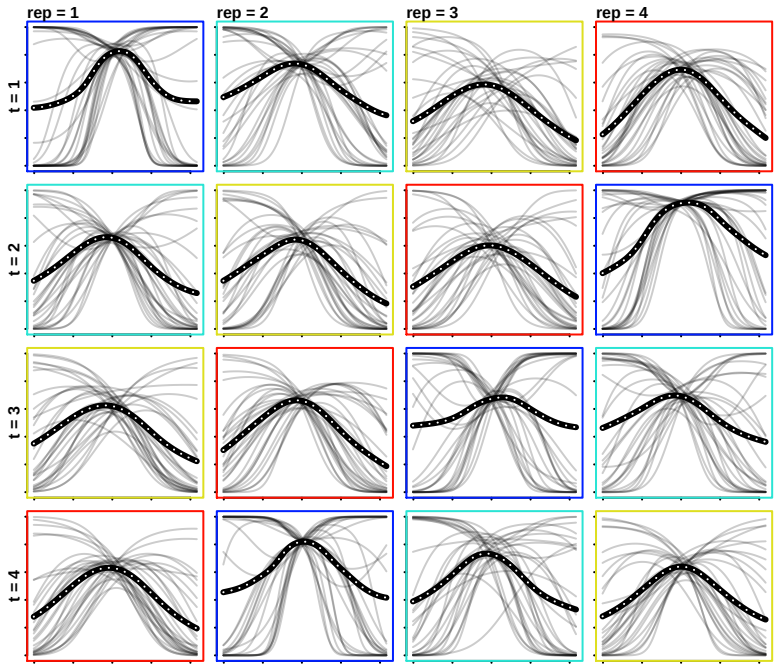

Figure 9: Response curves of species' probability of occupancy (ψ_i, vertical axis) across the full range of temperatures in the simulation. The color of the boxes around each panel refer to the among-species average of the probability of detection; warm colors indicate that the mean detection probability is high, whereas cool colors indicate that p was low. The year t of the simulated true process changes across the rows of panels, and the simulated replicate observation r changes across columns.

Probability of Detection, p

Definition of p

The probability of detection (p), is a species specific parameter in the MSOM model. The MSOM analyzes all years (t) and replicates (r) separately, so I am going to leave those subscripts out of this description. In the simulation, the probability of observing a species is a function of two independent factors:

1. The probability that site j is occupied by species i; this is $\psi_{j,i}$
    - $\psi_{j,i}$ is a function of species-specific niche and an environmental variable that changes over space and time
    - $Z_{j,i}$ is the species- and site-specific richness, which is a function of ψ (given that we're only talking about species that are in the pool of possible species, determined by w_i)
2. A species-specific (i) chance of being identified (`taxChance`), given that it is present in a location that was sampled (i.e., detectability does not reflect the probability of sampling a place); this detectability parameter is p_i
    - Detectability changed between years.
    - In a given year, $logit(p_i) \sim \mathcal{N}(\sqrt{}^{\mu}, \sigma^{\in})$. p_μ changed between years (taking on values of -2, 0, 2, and 4), $\sigma^2 = 2$ in all years.
    - The value of p only changes between species (and years), but the observation process occurs at the substratum (k) level. Thus, the parameter is really $p_{j,k,i}$, but for a given i, all $p_{j,k}$ are constant. I represent this probability as p_i with the understanding that this value is repeated over space.
    - $Y_{j,i}$ is the observed version of $Z_{j,i}$.
    - $Y_{j,i} \sim Bern(p_i \times Z_{j,i})$.
        - *Note: Because p is actually subscripted to k, the Y are also actually subscripted to k. Maybe leaving these subscripts out is making things more confusing. I've only excluded them to emphasize how parameters are estimated.*
    - Our data about species presence/ absence correspond to $Y_{j,i}$. So it might be useful to think of the MSOM as estimating $\hat{Y}_{j,i}$, which is compared to the observed data $Y_{j,i}^{obs}$.

Demo: Effect of MSOM Hierarchy on p

The above plot is interesting because it shows that exceptionally high or exceptionally low chances to be observed only occur for the species that were observed at least once; i.e., this says that if you didn't observe it, it just takes on the mean. That's reasonable, I guess; but I also would think that the things that were never observed could also be things that had a low chance of observability; but they could also have just a low chance of actually being present. So I suppose in the end it just doesn't get informed, and reverts to the mean?

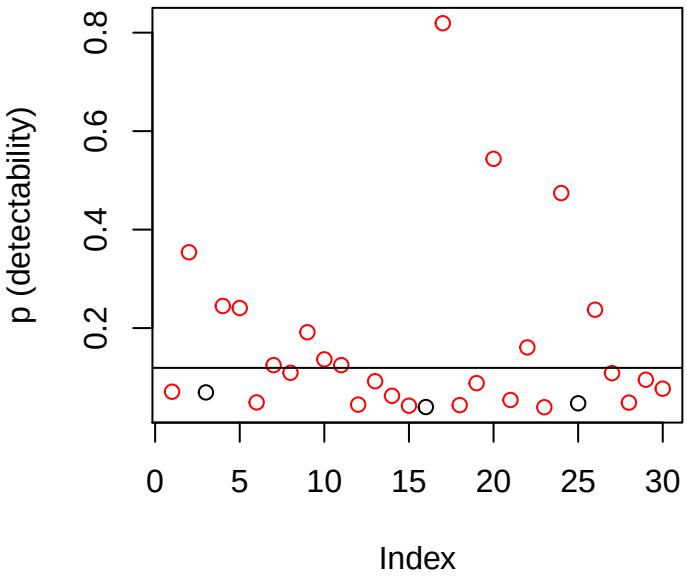

Figure 10: Probability of being detected, p. Horizontal line is mean probability. Figure only shows results for the first year of the simulation/ observation, and only 1 replicate. Different points are different species. Probability of being detected is a species-specific parameter (does not vary among sites, e.g.). Red points are species that were observed, black points are species that were never observed.

Scatter Plot of $\hat{p}$ vs p_{true}

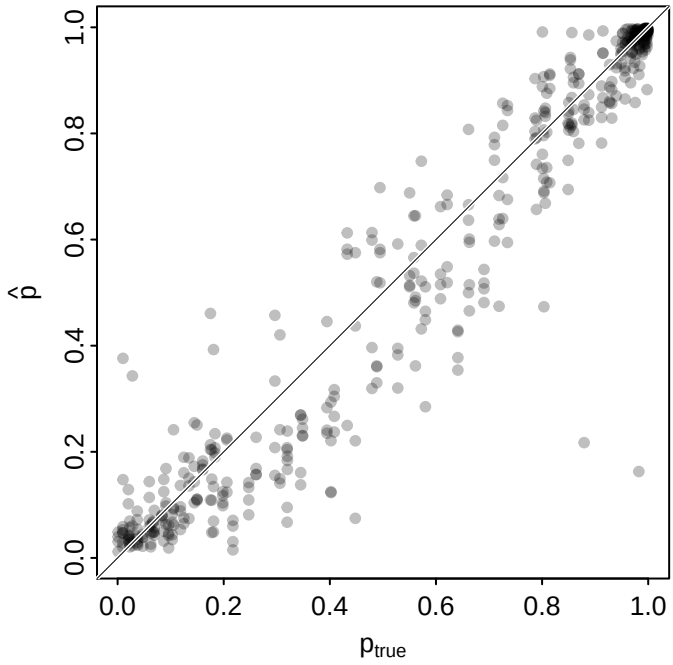

Figure 11: MSOM estimates (vertical axis) and true values of p_i, the species-specific (i) detection probability. Each point is subscripted by species i, year t, and observation replicate r.

Scatter Plot of $\hat{p}$ vs p_{true}, split by year and replicate

Text explanation goes here

Figure 12: Caption goes here.

Assessment with Mixed Effects Models

Describe Motivation for Mixed Effects Models

Motivation: MSOM skill might differ across dimensions, trying to figure out what patterns I should expect to pick out (spatial patterns in richness, temporal?) E.g., Is the correlation between MSOM and True the same comparing across sites as comparing across years? Species, reps, also.

Motivation: What factors influence MSOM skill in a given dimension? E.g., Skill in finding differences in ψ across species may depend on p, the chance of being identified. If p changes among years, might also explain

Read more about specifying mixed effects models using `lmer` in R here

This example is looking at ψ, probability of an individual species being present

Example LMER Analysis for ψ

```
# Just exploration/ starting point
library(car)
library(lme4)

blah <- reshape2:::melt.array(
    psi.true,
    varnames=c("site","spp","time","rep"),
    value.name="true",
    as.is=T
)

blah.hat <- reshape2:::melt.array(
    psi.hat,
    varnames=c("site","spp","time","rep"),
    value.name="hat",
    as.is=T
)

blah <- cbind(blah, hat=blah.hat[,"hat"])

blah$site <- as.factor(blah$site)
blah$spp <- as.factor(blah$spp)
blah$time <- as.factor(blah$time)
blah$rep <- as.factor(blah$rep)
```

```
# ====================
# = Do LMER Analysis =
# ====================
(blah.mod <- lmer(hat~true+(1|spp)+(1|time), data=blah))
```

```
## Linear mixed model fit by REML ['lmerMod']
## Formula: hat ~ true + (1 | spp) + (1 | time)
##    Data: blah
## REML criterion at convergence: -7303.128
## Random effects:
##  Groups   Name        Std.Dev.
##  spp      (Intercept) 0.04946
##  time     (Intercept) 0.02326
##  Residual             0.21984
## Number of obs: 38880, groups:  spp, 30; time, 4
## Fixed Effects:
## (Intercept)         true
##      0.1201       0.8734
```

```
Anova(blah.mod)
```

```
## Analysis of Deviance Table (Type II Wald chisquare tests)
##
## Response: hat
##      Chisq Df Pr(>Chisq)
## true 34126  1  < 2.2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
# ================
# = Explain LMER =
# ================
```

Report Generation Notes

R Session Information

```
## R version 3.2.0 (2015-04-16)
## Platform: x86_64-apple-darwin13.4.0 (64-bit)
## Running under: OS X 10.10.5 (Yosemite)
##
## locale:
## [1] en_US.UTF-8/en_US.UTF-8/en_US.UTF-8/C/en_US.UTF-8/en_US.UTF-8
##
## attached base packages:
## [1] parallel  grid      stats     graphics  grDevices utils     datasets
## [8] methods   base
##
## other attached packages:
##  [1] lme4_1.1-9       Matrix_1.2-0     car_2.0-26       kfigr_1.2
##  [5] xtable_1.7-4     rmarkdown_0.7    knitr_1.11       doParallel_1.0.8
##  [9] iterators_1.0.7  foreach_1.4.2    R2jags_0.5-6     rjags_3-15
## [13] coda_0.17-1      igraph_0.7.1     fields_8.2-1     maps_2.3-9
## [17] spam_1.0-1       data.table_1.9.4 raster_2.3-40    sp_1.1-0
## [21] rbLib_0.0.2      taxize_0.5.2
##
## loaded via a namespace (and not attached):
##  [1] reshape2_1.4.1   splines_3.2.0    lattice_0.20-31  htmltools_0.2.6
##  [5] yaml_2.1.13      mgcv_1.8-6       chron_2.3-45     XML_3.98-1.3
##  [9] nloptr_1.0.4     plyr_1.8.2       stringr_1.0.0    codetools_0.2-11
## [13] evaluate_0.7.2   Taxonstand_1.7   SparseM_1.7      permute_0.8-4
## [17] quantreg_5.11    pbkrtest_0.4-2   numbers_0.6-1    highr_0.5
## [21] Rcpp_0.11.6      formatR_1.2      vegan_2.3-0      jsonlite_0.9.16
## [25] abind_1.4-3      digest_0.6.8     stringi_0.5-5    ssh.utils_1.0
## [29] tools_3.2.0      bitops_1.0-6     magrittr_1.5     RCurl_1.95-4.6
## [33] bold_0.2.6       cluster_2.0.1    ape_3.3          MASS_7.3-40
## [37] minqa_1.2.4      assertthat_0.1   reshape_0.8.5    httr_0.6.1
## [41] boot_1.3-16      R2WinBUGS_2.1-21 nnet_7.3-9       nlme_3.1-120
```

Date Document Last Compiled

```
## Last compiled on:  2015-08-25
```
