Improving Catch Estimation Methods in Sparsely Sampled Mixed-Stock Fisheries.

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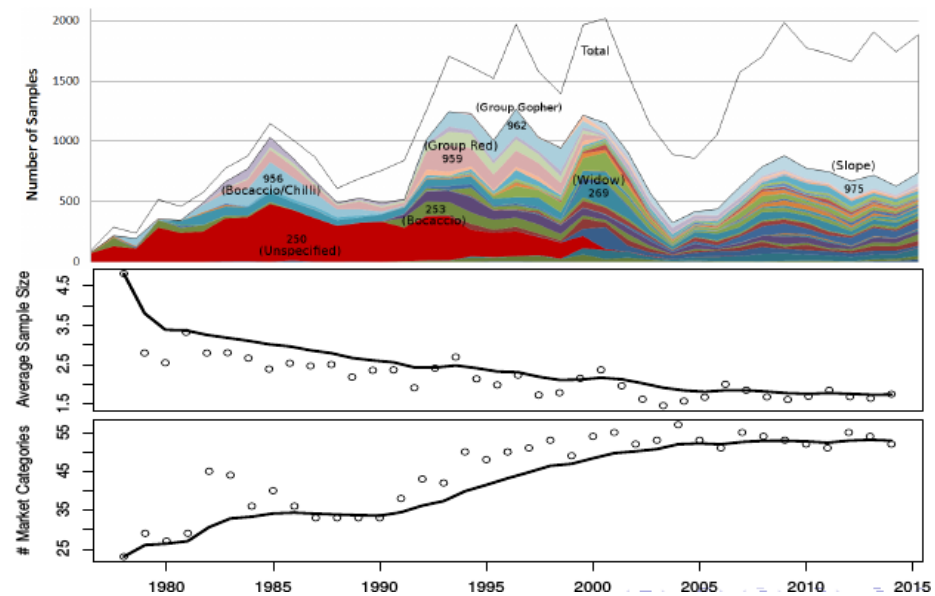## Abstract

Introduction

Context

Figure 1: Spase Data

Methods

Data

As outlined in (*cite*) the data in *blank* are the result of a cluster sampling protocol across the many strata, in which each sample is intendeded to be composed of two fifty pound clusters from the selected stratum. Although port samplers do there best to follow protocol, in reality the port sampling environment does not always allow the exact (*cite*) protocol to be followed. Variations in the sampling protocol may result in more or less clusters taken, or the size of clusters taken to vary, from stratum to stratum based on the particular challanges of sampling each stratum.

The model based methodology proposed here does not rely strongly upon the cluster sampling structure, but rather simply views each sample as independent and identically distributed (*I.I.D.*) draws from some data generating model, conditional on some parameterisation of the stratification system. So long as the parameterisation and data generating model are sufficiently robust for handeling the quirks of these data in particular, the conditionally *I.I.D.* model of these data can be seen as practically useful for producing predictions about the data generating system even if our model does not replicate the true data generating process exactly.

That said, for the purpose of building models of these data it is enough to know which clusters were collected as part of which samples, and how big each cluster actually ended up being. This information is readily available from CALCOM. For the purpose of the models presented here, all of the observed clusters across a unique sample are aggregarted so that the total weight sampled is the sum of all of the total pounds sampled in each cluster of each unique sample. Similarly the observed weight for a particular species in each unique sample is the sum of all of the observed weights, for that species, across each cluster of each unique sample.

Although model based data analysis has the potential to add significant structure to data, an ethical application of these methods must always confront the model with enough emperical information to adequatly learn about the system. In this setting some market categories and time periods may not be well enough sampled to learn the parameters of the models presented here. For any modeled period where the minimum number of possible parameters exceeds the number of samples for the modeled period, the model is not applied. Rather than apply models inappropriatly, these cases are speciated as the nominal species for their market category. We later demonstrate in Figure (*bars*) that due to the prioritization for sampling heavily landed, or otherwise commercially realavent categories, a sample size heuristic such as this typically only leads to nominal speciation in market categories and time periods where total landings are low. Thus the expanded landings in these periods have a negligable effect on the

overall expanded landings for species in these categories.

Data Generating Model

Something something heirarchical poisson model. Something something (Shelton, 2012).

For the purposes of accurately modeling not only species composition means, but also higher moments of the data, such as species composition variances, it is neccisary to recognize model limitations with respect to over-dispersed data. Amoung the simplest models for count data are the poisson and binomial models. Both models are typically specificed with a single parameter for modeling all of the moments of the data, and thus they rely heavily on their respective data generating processes to accurately represent higher moments in the data. McCullagh and Nelder (1989, pg. 124) commiserate about the prevalence of over-dispersed data in cluster sampling, and explain ways in which cluster sampling itself may result in over-dispersion.

Extending the Poisson and binomial models to deal with over-dispersion, typically involves adding additional parameters for the purpose of modeling higher moments of the data. The negative binomial (NB) distribution is often used as an over-dispersed extension of the poisson model, since it can be expressly written as an infite mixture of poisson distributions. While the beta-binomial model is typically used to as an over-dispersed extension of the binomial model.

An Example

To discern between these discrete modeling options we consider a small scale example of the Poisson, binomial, negative binomial, and beta-binomial models fit to the port sampling integer weight data from market category 250, in the Montery port complex trawl fishery in 1982. (*anywillwork*) This stratum was visited 32 times by port samplers, collecting a total of 59 cluster samples across 55 unique species. Each of the above models are fit to these data.

The Poisson and binomial models attempt to model both the mean and residual variance of the data with a single parameter for each species. By definition these models have residual varinces which are tied to the species means. Simply estimating the mean parameters in these cases may not be sufficient to produce models which predict well.

In contrast, the negative binomial and beta-binomial models estimate an additional parameter which can be used to disentangle the mean and residual variance estimates. Thus the negative binomial and beta-binomial models may produce more accurate estimates of the residual variance. Furthermore, in better modeling the variance, these models may often prduce more accurate measures of center as well.

For each of the above mentioned models The predictive species composition distributions are visualized in Figure($IntervalPlot$) as 95% Highest Density Intervals (HDI) ($citations$), plotted on top of the predictive means for each model and the observed species compositions from the data in Figure($IntervalPlot$). For brevity we only consider the most prevalent six species in this example (CLPR, BCAC, WDOW, BLGL, ARRA, BANK). Additionally, the MSE, DIC, WAIC, and Bayesian marginal likelyhood model probabilities are computed for each model as measures of model fit as seen in Table($likelihoodtable$).

Table($likelihoodtable$) show a clear preference for the overdispersed models, with the most overall support for the beta-binomial model. This initial result guides the use of the beta-binomial data generating model for the purposes of building a model to apply at an operational scale.

Operationalized Model

For a particular market category, $y_{ijklm\eta}$ is the ith sample of the jth species' weight, in the kth port, caught with the lth gear, in the ηth quarter, of year m. As supported by the preliminary results in Figure($IntervalPlot$) and Table($likelihoodtable$), the $y_{ijklm\eta}$ are modeled as observations from a beta-binomial distribution conditional on parameters $\mu_{jklm\eta}$ and $\sigma^2_{jklm\eta}$,

$$y_{ijklm\eta} \sim BB(\mu_{jklm\eta}, \ \sigma^2_{jklm\eta}).$$

Where $\mu_{jklm\eta}$ is the stratum level beta-binomial mean weight and $\sigma^2_{jklm\eta}$ is the stratum level residual variance. $\mu_{jklm\eta}$ is related to a linear predictor, $\theta_{jklm\eta}$, via the mean function,

$$\mu_{jklm\eta} = n_{ijklm\eta} \frac{\exp(\theta_{jklm\eta})}{1 + \exp(\theta_{jklm\eta})} = n \ \text{expit}(\theta_{jklm\eta}) = n \ \text{logit}^{-1}(\theta_{jklm\eta}).$$

Here $n_{ijklm\eta}$ is the observed aggregate cluster size for each sample. Additionally, $\sigma^2_{jklm\eta}$ is related to $\mu_{jklm\eta}$ and the overdispersion parameter, ρ, via the following equation,

$$\sigma^2_{jklm\eta} = \mu_{jklm\eta} \Big(1 - \frac{\mu_{jklm\eta}}{n_{ijklm\eta}}\Big) \Big(1 + (n_{ijklm\eta} - 1) \ \rho\Big).$$

ρ is the within cluster correlation. The situation where $\rho \to 1$ represents identical information content amoung replicates within a cluster, with maximal overdispersion relative to the binomial distribution. The situation where $\rho \to 0$ represents totally independent information content amoug replicates within a cluster, and the beta-binomial model approaches the binomial model. ρ explicitly

models average overdispersion across all stratum, while $\mu_{jklm\eta}$ gives the model flexiblity at the stratum level through the θ linear predictors,

$$\theta_{jklm\eta} = \beta_0 + \beta_j^{(s)} + \beta_k^{(p)} + \beta_l^{(g)} + \beta_{m\eta}^{(t)}.$$

Firstly, θ includes a reference level intercept (β_0). Secondly, θ is factored among the many strata by additive offsets from β_0 for each of the species ($\beta_j^{(s)}$), port-complex ($\beta_k^{(p)}$), and gear-group ($\beta_l^{(g)}$) categories. Finally year and quarter parameters are indicated generally here inside the $\beta_{m\eta}^{(t)}$ term. Several forms for $\beta_{m\eta}^{(t)}$ are explored each implying a different prior and partial pooling strategies as described in the following section($Priors$).

Priors

To complete the bayesian formulation of this model, priors are expressed in a largly diffuse manner.

$$\beta_0 \propto 1$$
$$\left\{ \beta_j^{(s)}, \beta_k^{(p)}, \beta_l^{(g)} \right\} \sim N(0, 32^2)$$

Since the β_0 reference level is choosen arbitarily, with no conception of which values it may take, no restrictions are placed on the value of the intercept. The species ($\beta_j^{(s)}$), port-complex ($\beta_k^{(p)}$), and gear-group ($\beta_l^{(g)}$) offsets are assigned diffuse normal priors. The large fixed values of the prior variance hyperparameters produce behavior similar to classical fixed effect models for species, port-complex, and gear- group parameters.

In returning to the time parameter model, $\beta_{m\eta}^{(t)}$, it is useful to consider how the inclusion of predictively superfluous parameters may cause overfitting and weaken model performance through the bias-variance dilemma (Ramasubramanian, K., & Singh, A., 2016). Simply put, the bias-variance dilemma means that model formulation is not simply a bias reduction task, but rather the goal is to formulate models which reduce bias, while jointly minimizing uncertainty. Janyes (2003, pg. 511) describes how the inclusion of estimation bias via the Bayesian methodolgy may produce better performing estimates, more quickly, than unbiased counterparts. Amoung the simplest ways to see the principle is in the structure of the MSE performance metric, and how it can be explicitly written to value both estimator bias and variance, as follows.

$$\mathrm{MSE}(\hat{\theta}) = \mathbb{E}\left[(\hat{\theta} - \theta)^2 \right] = \overbrace{\mathbb{E}\left[\left(\hat{\theta} - \mathbb{E}(\hat{\theta})\right)^2 \right]}^{\mathrm{Var}(\hat{\theta})} + \overbrace{\left(\mathbb{E}(\hat{\theta}) - \theta \right)^2}^{\mathrm{Bias}(\hat{\theta},\theta)^2}$$

Furthermore a model can mimimize bias, without reguard for estimation uncertainty, by including one model parameter to be fit to each observation. These parameter estimates are totally unbiased, however such a model is also predictively usless since each estimated parameter is specifically bound to a particular observation, and thus such a model does not generalize.

For modeling $\beta_{m\eta}^{(t)}$ we consider a spectrum of models which span a wide range of partially pooled models with several different predictive structures as seen below.

(M1)

$$\beta_{m\eta}^{(t)} = \beta_m^{(y)} + \beta_\eta^{(q)}$$

$$\beta_m^{(y)} \sim N(0, 32^2)$$

$$\beta_\eta^{(q)} \sim N(0, 32^2)$$

(M1) represents a fixed effects model for additive year and quarter parameters. Here each year and quarter receive totally independent and diffuse priors.

(M2)

$$\beta_{m\eta}^{(t)} = \beta_m^{(y)} + \beta_\eta^{(q)}$$

$$\beta_m^{(y)} \sim N(0, v^{(y)})$$

$$\beta_\eta^{(q)} \sim N(0, v^{(q)})$$

(M2) estimates two heirarchical variance parameters, $v^{(y)}$ and $v^{(q)}$. $v^{(y)}$ has the effect of partially pooling information among year parameters, while $v^{(q)}$ partially pools information among quarter parameters. The actual degree of pooling among each of the years and quarters is determined by the data. Depending on the posterior distributions of $v^{(y)}$ and $v^{(q)}$, $\beta^{(y)}$ and $\beta^{(q)}$ may be shrunk back toward the common mean for small v or allowed to take largely distinct values in the case of large estimates of the v.

(M3)

$$\beta_{m\eta}^{(t)} = \beta_m^{(y)} + \beta_\eta^{(q)} + \beta_{m\eta}^{(y:q)}$$

$$\beta_m^{(y)} \sim N(0, v^{(y)})$$

$$\beta_\eta^{(q)} \sim N(0, v^{(q)})$$

$$\beta_{m\eta}^{(y:q)} \sim N(0, v)$$

(M3) functions similarly as (M2), in that it has heirarchical partial pooling among both the $\beta_m^{(y)}$ and $\beta_\eta^{(q)}$ parameters, except that it intoduces a two-way interaction term between year and quarter. This interaction term allows estimates for particular quarters to differ from year to year, as opposed to the previous models in which quarters within a year are assumed to be identical from year to year.

Furthermore the $\beta_{m\eta}^{(y:q)}$ are also modeled heirarchically to introduce a single variance parameter, v, shared among all of the $m\eta$ time chunks. Although this interaction term adds many parameters to the model, the shared v parameter functions to shrink extranious $\beta_{m\eta}^{(y:q)}$ estimates back toward the common stratum mean.

(M4)

$$\beta_{m\eta}^{(t)} = \beta_{m\eta}^{(y:q)}$$

$$\beta_{m\eta}^{(y:q)} \sim N(0, v)$$

(M4) simplifies (M3) by excluding year and quarter main effects. This leaves all temporal information in the data to be modeled solely by the quarterly $\beta_{m\eta}^{(y:q)}$ interaction terms. This model reqresents more opportunity for partial pooling through time than (M3), as fewer time parameters are introduced. Furthermore all of the $\beta_{m\eta}^{(y:q)}$ are heirarchically pooled back toward a single common stratum mean via the single shared variance parameter, v.

(M5)

$$\beta_{m\eta}^{(t)} = \beta_{m\eta}^{(y:q)}$$

$$\beta_{m\eta}^{(y:q)} \sim N(0, v_\eta)$$

(M5) is largely the same as (M4), but it represents slightly less potential partial pooling through its heirarchical prior variances, v_η, on $\beta_{m\eta}^{(y:q)}$. Here interaction terms are allowed to partially pool interactions across years, within a common quarter, but since each quarter is assigned a separate variance parameter no pooling is possible between quarters.

(M6)

$$\beta_{m\eta}^{(t)} = \beta_{m\eta}^{(y:q)}$$

$$\beta_{m\eta}^{(y:q)} \sim N(0, v_m)$$

(M6) follows the same idea as (M5), however here interaction terms are allowed to partially pool interactions within a common year, across the quarters of that year, but not between years. (M6) often involves fitting slightly more parameters than (M5) because, at least in this setting, it is typical to model more than four years of data at once.

Heirarchical variance parameters are estimated from the data. As the above models learn the posteriors of the hierarchical variance parameters, it affects the degree of shrinkage as well as the effective number of parameters held within the respective heirarchies (Gelman, 2014). To achieve this, each variance parameter must itself be assigned a prior to be estimated. For all of the heirarchical variance parameters included in the above models v is assigned a diffuse $v \sim IG(1,\ 2 \times 10^3)$ prior.

Finally the overdispersion parameter, ρ, is assigned a diffuse normal prior on the logit scale, $\text{logit}(\rho) \sim N(0, 2^2)$. The $N(0, 2^2)$ prior is indeed a symmetric, and far reaching, prior when back transformed to the unit interval. To notice this, it is helpful to realize that the central 95% inverval for a $N(0, 2^2)$ (i.e. 0 ± 3.91), includes almost the entirety of the back transformed unit interval (i.e. 0.5 ± 0.48).

Table($priortable$) shows a clear preference for model (M4). It is worth mentioning that amoung all of the models considered here, (M4) offers the largest potential for heirarchical partial opooling amoung the time parameters. For the duration of the methods we build upon this preliminary result.

Species Composition Prediction

Estimating model (M4) in a Bayesain way gives access to the full posterior distribution of all of the parameters of the model. It is useful to emphasize that in the Bayesian setting, these parameters have full distributions, and they are typically handeled as a large number of samples from the joint posterior distribution of the parameters. Once the posterior sampling is complete, this simplifies parameter mean and variance estimation since the required moments are simply obtainted by computing the desired moments from the posterior samples. Additionally the fact that the parameters are full distributions, means that any functions which contain, or are derived from, parameters are themselves random variables with the function representing a random variable transformation of those parameters.

To obtain predicted species compositions from this model, first consider the posterior predictive distribistion of sampled weight for a particular stratum.

$$p(y^*_{jklm\eta}|y) = \iint \text{BB}\Big(y^*_{jklm\eta}|\mu_{jklm\eta}, \sigma^2_{jklm\eta}\Big) P\Big(\mu_{jklm\eta}, \sigma^2_{jklm\eta}|y\Big) d\mu_{jklm\eta} d\sigma^2_{jklm\eta}.$$

Here BB is the data generating beta-binomial distribution for a predictive observation and $P(\mu_{jklm\eta}, \sigma^2_{jklm\eta}|y)$ is the posterior distribution of the parameters given the observed data. Integration of the parameters, $\mu_{jklm\eta}$ and $\sigma^2_{jklm\eta}$, is done by monte carlo integration to obtain samples from the predictive distribution, $p(y^*_{jklm\eta}|y)$, for sampled weights in the $jklm\eta^{th}$ stratum.

Obtaining predictive species compositions from predictive weights amounts to computing the following transformation,

$$\pi^*_{jklm\eta} = \frac{y^*_{jklm\eta}}{\sum_j y^*_{jklm\eta}} \quad y^*_{klm\eta} \neq 0.$$

Here $\pi^*_{jklm\eta}$ is the models representation of the observation level species composition for species j in the kth port, caught with the lth gear, in the ηth quarter, of year m.

Model Exploration & Averaging

Presently, stratum with deminishingly small sample sizes are managed by an ad-hoc "data borrowing" protocol, as outlined in Pearson and Erwin (1997). The protocol for "data borrowing" calls for pooling only when forced to fill holes brought about by unsampled strata. Naturally, such a pooling protocol introduces bias to fill in unsampled strata, however due to the mathematically unstructured way in which this bias is introduced, it is hard to quantitatively justify these "data borrowing" rules.

Model (M4) avoids temporal ad-hoc "borrowing" protocols used in Pearson and Erwin (1997) by making use of its heirarchical structure to fill temporal holes with a posterior predictive distribution for unseen time periods within the modeled period. This heirarchical structure uses the data to estimate the degree of pooling through time, rather than ad-hoc "data borrowing".

Despite the benefits of modeling these data as Bayesian heirarchical models, port sampling data still remains sparce. Given the degree of sparcity in these data it is certainly possible that models which consider an additional degree of data pooling between port complexes may offer predictive benefits. In exploring strategies for pooling data across space it is necessary to formalize the port complex pooling scheme in a way which provides a mathematically understandable and scalable structure to build upon.

Given the categorical nature of port complex variables, the typical heirarchical regularization priors amoung port complexes are not appropriate. Rather, we frame port complex pooling as a model uncertainty problem, in which we consider some degree of port complex pooling, but the exact degree of pooling, and the particular partitioning of the pooled port complexes are not known.

Port complex pooling is achieved by repeatedly fitting model (M4) with different partitionings of the port complex variables within a particular market category and modeling time period. This model exploration exercise explores the possible ways to produce groupings of the existing port complexes so as to discover predictively useful partionings of the port complexes. Insisting that the port complex groupings be partitions of the availiable port complexes provides a well defined mathematical structure for exploring the space of pooled port complexes.

The size of the space of possible pooled models is in the setting is well defined in terms of the size of the set of items to be partitioned, K, as given by the Bell numbers (B_K),

$$B_K = \sum_{\hat{k}=0}^{K} \frac{1}{\hat{k}!} \left(\sum_{j=0}^{\hat{k}} (-1)^{\hat{k}-j} \binom{\hat{k}}{\hat{j}} j^K \right).$$

In the case of California the set of items to be partitioned is the set of port complexes in California, of which there are $K = 10$, implying a grand total of $B_{10} = 115975$ ways of partitioning the port complexes in California in each market category and modeled time period. The brute force model selection strategy of computing all 115975 of these partitionings strategies is computationally infeasible. However, not all pooling schemes represent biologically relevant models. For example, perhaps it is reasonable to pool only among adjacent ports (i.e. no discontinuities between port complex pooling in space), or perhaps it is reasonable to assert that biologically similar regions can only extend across a small number of ports.

Here only adjacent port poolings are considered, such that the maximum size of a port complex grouping is three port complexes. These are the only two constraints that are enforced on port complex partitions here, although many other constraints may, in theory, be chosen. These constraints were chosen so as to mirror the currently accepted protocols in Pearson and Erwin (1997) within the context of this framework. When these two simple constraints are applied, the number of models to explore in each modeled period is reduced to a much more manageable 274 models.

An exhaustive search of the models in the biologically constrained subspace of B_{10}, allows for a concrete comparison of the relative predictive accuracy of each partitioning. Additionally the partitioned models provide a set of candidate models for use in Bayesian Model Averaging (BMA) (Hoeting et al., 1999). BMA, as applied here, essetially allows the model exploration strategy to average across all realavent port complex partionings and adds robustness to the final species composition estimates.

For the ιth model in a set of candidate models M, then the BMA weight for M_ι follows directly from Bayes Theorem as,

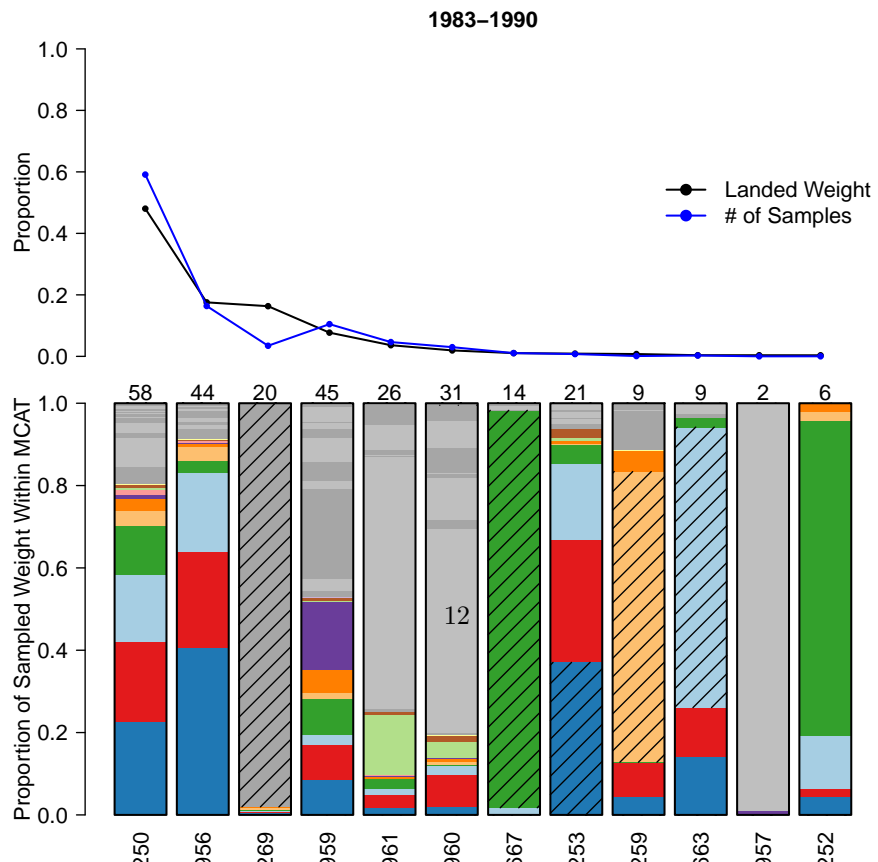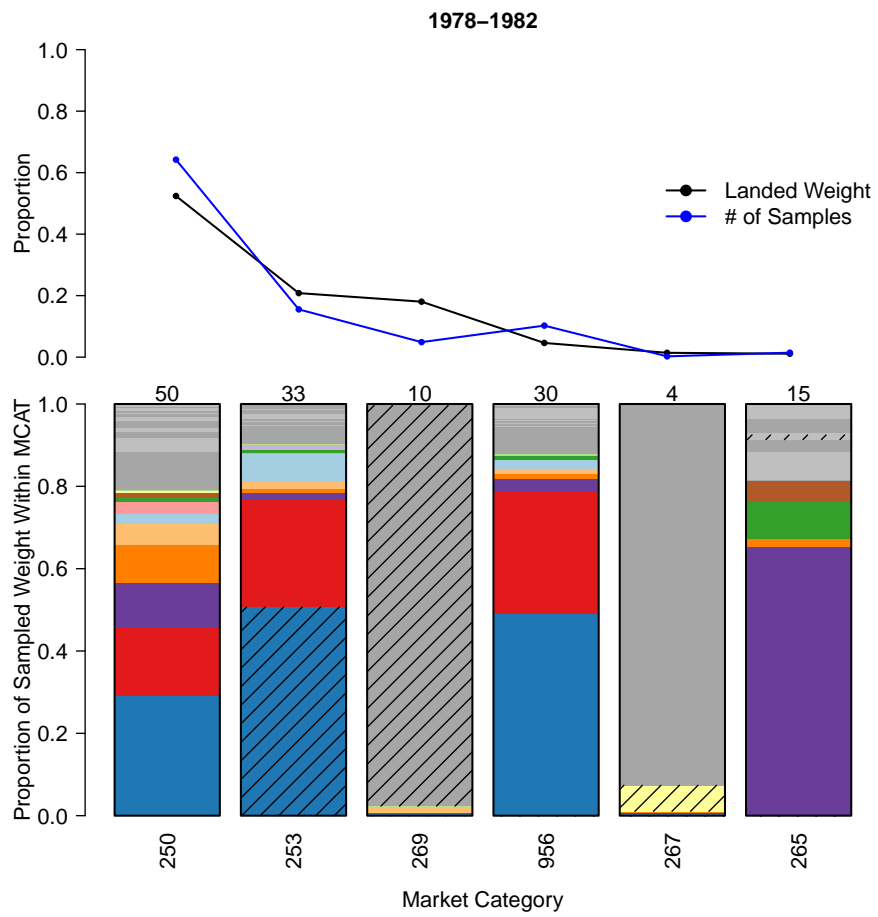$$\omega_\iota = Pr(M_\iota|y) = \frac{p(y|M_\iota)p(M_\iota)}{\sum_\iota p(y|M_\iota)p(M_\iota)}.$$

Where ω_ι is the posterior probability that model ι is the true data generating model of the data, conditional on the subspace of candidate models and the observed data. ω_ι is then straightforwardly used to average posteriors across all of the models, as

$$\bar{p}(\theta|y) = \sum_\iota \omega_\iota p(\theta|y, M_\iota).$$

Results

Data

Figure ($bars$) shows the relative sampling effort and landings across the top x percent of landed rockfish market categories for two modeled periods. In the top panel of each modeled period the black line represented the proportion of landings in each market category, while the blue line represents the proportion of samples, by number, taken in each market category. In the bottom panel of each modeled period, colors repesent the proportion of sampled weight of the top twelve most landed species in the port samples. Alternating dark and light grey panels fill in all other species. On the top of each bar are the number of observed species in each market category. Hatched regions indicated the nominal species of a market category where applicable.

1978–1982

Proportion

- Landed Weight
- # of Samples

Proportion of Sampled Weight Within MCAT

| 50 | 33 | 10 | 30 | 4 | 15 |

250   253   269   956   267   265

Market Category

1983–1990

Proportion

- Landed Weight
- # of Samples

Proportion of Sampled Weight Within MCAT

| 58 | 44 | 20 | 45 | 26 | 31 | 14 | 21 | 9 | 9 | 2 | 6 |

250   956   269   959   961   960   967   253   959   963   957   952

- BANK
- BCAC
- ARRA
- BLGL
- BLCK
- CLPR
- YTRK
- CNRY
- BLUR
- VRML
- BRWN
- RDBD

Data Generating Model

Example

Table(1) shows model performance metrics for the toy example considered from market category 250 for the Montery Trawl fishery in 1982. Here we consider Mean Squared Error (MSE; computed on the species composition scale), deviance information criterion (DIC), widely applicable information criterion (WAIC), and marginal bayesian model probabilities ($pr(M|y)$). These measures span a wide range of model selection philosphies and yet here they all consistently agree in ranking the likelihood models. Both of the overdispersion models considered here (NB and BB) outperform the more standard Poisson and binomial count models, with the most support being for the BB model and the Piosson model showing the least support.

	Poisson	Binomial	NB	BB
MSE	0.06412	0.06264	0.05171	0.04479
DIC	1342.27	1571.46	345.89	340.86
WAIC	1421.61	1665.41	345.09	341.66
$pr(M|y)$	≈ 0	≈ 0	$\approx 10^{-7}$	≈ 1

Figure(1) shows observed species compositions plotted against Poisson, Binomial, NB, and BB predictive intervals. Here 95% highest density intervals (HDI) are shown to visualize the predictive accuracy of each model against the data.

The large spread of the observed species compositions seen in Figure(1) visually demonstrate the degree of overdispersion present in port sampling data. The Poisson and binomial models disregaurd this overdispersion to prioritize fitting the data mean. The NB and BB models explicitly model overdispersion in the data, albeit via differing mechanisms, and as such they predict a larger subset of the data.

The split beta-binomial intervals seen in Figure(1) are the consequence of confining a large amount of residual variability to the unit interval. The beta-binomial is the only model considered here, which estimates such a large degree of variablility and thus it is the only model that produces predictive species composition distributions of the sort. Figure(2) shows the beta-binomial predictive distributions as a violin plot demonstrating how the beta-binomial model arranges predictive density over the unit interval. The predictive intervals in Figure(1) are the smallest possible regions on each of these densities so that each intervals contain 95% probability. Species composition is bounded on [0, 1], thus in the presence of large variablity predictive density may aggragate around the bounds. For the example of STRK, notice that although the predictive HDI is split, the vast majority of density lies directly atop the data.
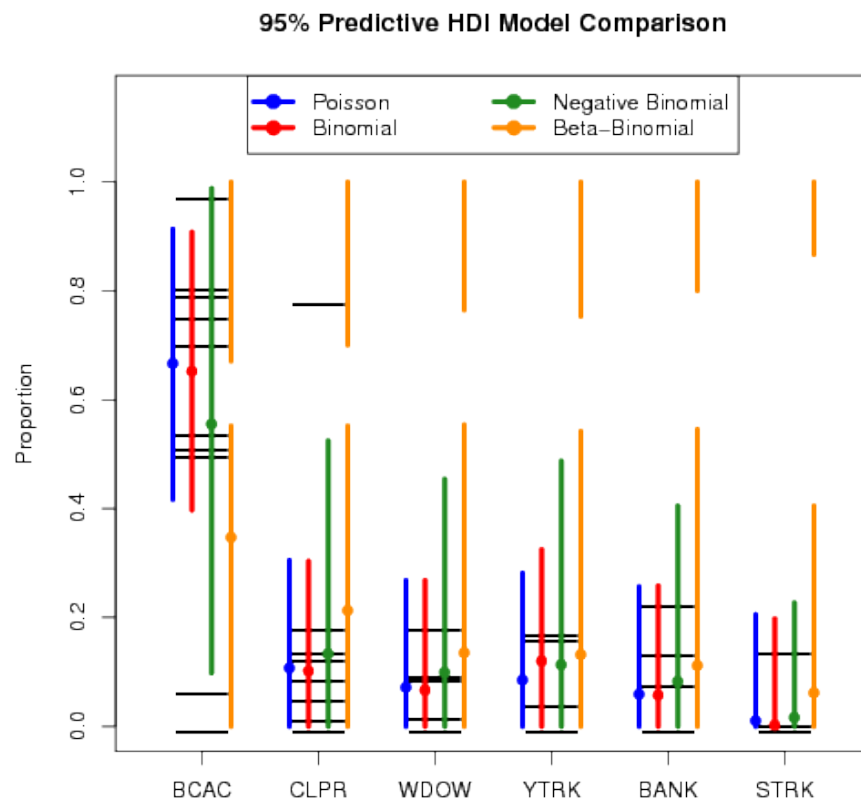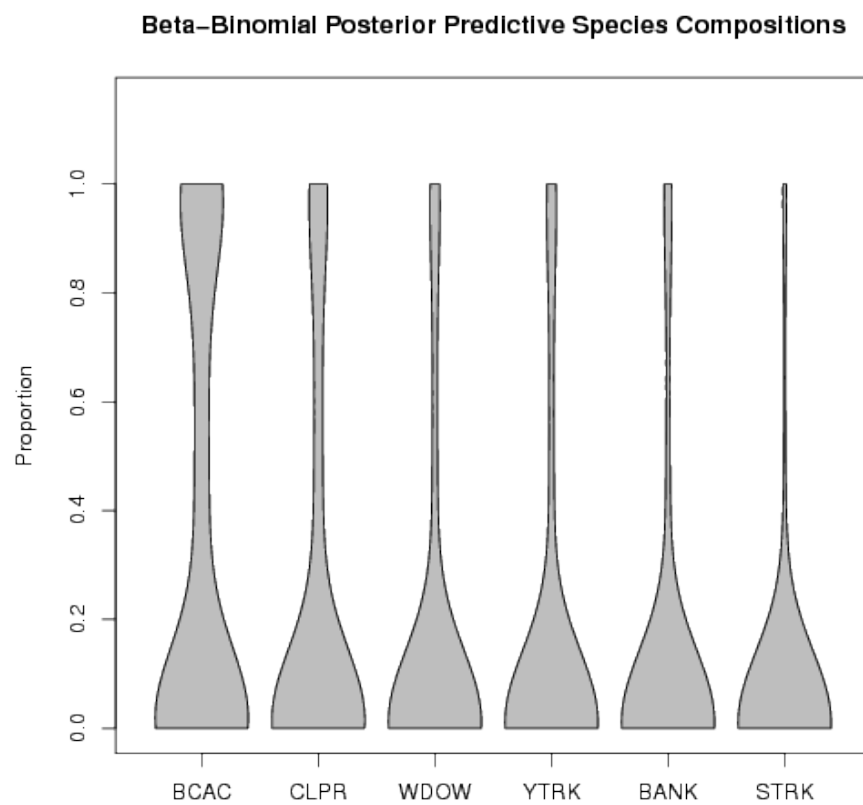
Figure 2: Interval Plot

Figure 3: Violin Plot

Predictor and Prior Selection

	M1	M2	M3	M4	M5	M6
MSE	0.127245	0.127042	0.126801	0.122373	0.127236	0.126573
DIC	39790.26	39491.64	39244.91	37231.70	39407.02	39406.41
WAIC	39745.58	39446.51	39192.25	37182.93	39354.11	39353.49
$pr(M|y)$	≈ 0	≈ 0	≈ 0	≈ 1	≈ 0	≈ 0

Table(XX) displays the relative support for the model structure on the $\beta_{m\eta}^{(t)}$ time parameters. From M1 to M4 the models represent a spectrum of models with an increasing potential of shrinkage among time parameters. Models M5 and M6 represent models which build in complexity, from M4, via the inclusion of multiple heirarchical variance parameters amoung the interaction terms.

Across all of the time models, model M4 displays consistent support over all other candidate models considered here. Model M4 represents a model with maximal potential for pooling through time, while still maintaining the ability to model differences in seasonality from year to year.

As a final check of the model structure and the implied prior information the prior predictive is considered. The prior predictive distribution summarizes the information that is intrinsic to the model structure itself, in the absense of data. The prior predictive of modeled weight is considered over a 100 pound cluster size, which is consistent with aggregating the two nominal 50 pound cluster samples described by Sen (1984) in the original sampling protocol.

As seen in Figure(XX) the prior predictive of (M4) is both symmetric and quite diffuse over the 100 pound domain. The U shape of the distribution is a side effect of the diffusion of the selected prior. As data are added to the model, the indecisive U shape of this distribution collapses toward the data in the posterior.

Model Exploration & Averaging

- One good model selection example
    - Maps?
- Include all results as table (fill in extra mcats)
- Fill in final prediction table values
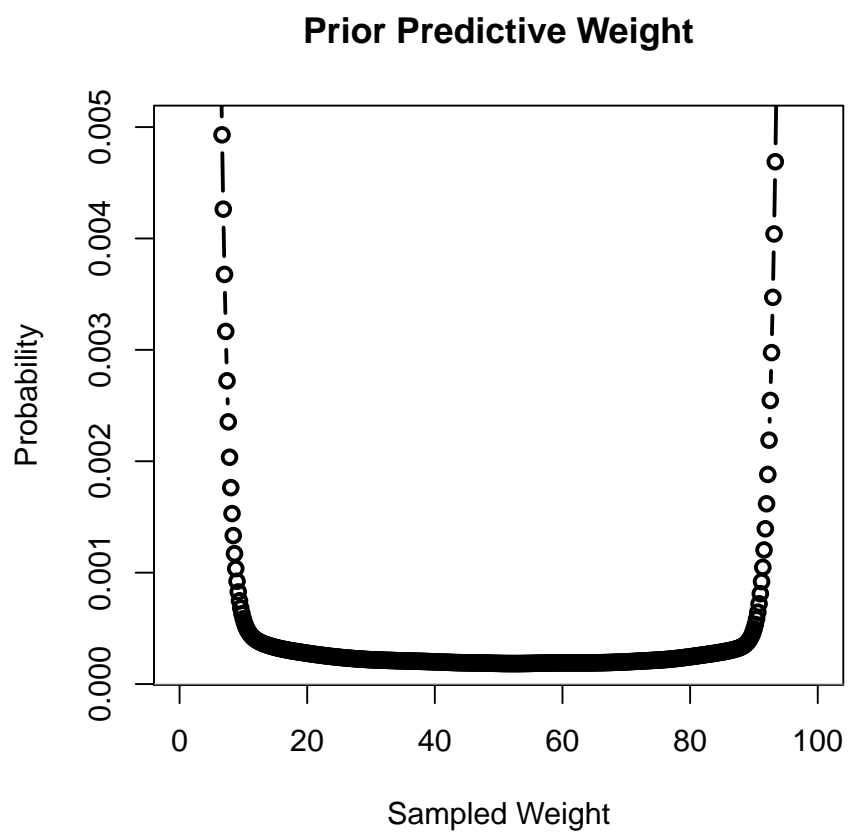
Prediction

- Should any of these be excluded?

Prior Predictive Weight

Figure 4: Prior Prediction

78-82

	68%	95%	99%
250	67.1%	96.1%	98.7%
253	67.3%	96.3%	98.9%
262	67.4%	93.8%	95.3%
265	69.6%	96.0%	97.8%
269	68.2%	88.8%	90.2%
270	68.6%	93.6%	96.7%
956	68.3%	96.7%	99.2%
959	68.5%	96.3%	98.1%
961	69.3%	93.2%	95.3%

83-90

	68%	95%	99%
245	60.8%	94.9%	97.7%
250	68.1%	96.0%	99.0%
253	69.3%	97.1%	98.9%
259	83.8%	91.9%	92.9%
262	68.5%	95.1%	95.9%
269	68.6%	94.2%	94.7%
270	67.9%	94.2%	96.7%
663	68.1%	94.1%	96.3%
667	69.4%	92.5%	93.5%
956	67.5%	96.2%	99.0%
959	67.4%	96.4%	99.0%
960	68.0%	96.1%	98.6%
961	68.6%	94.6%	97.8%

Nusiance Parameters

78-82

ρ

MCAT	Mean	Median	Posterior SD
250	0.55	0.55	0.004
253	0.39	0.39	0.001
262	0.35	0.35	0.008
265	0.64	0.64	0.002
269	0.52	0.52	0.019
270	0.53	0.54	0.020
956	0.35	0.35	0.007
959	0.47	0.47	0.070
961	0.55	0.55	0.004

v

MCAT	Mean	Median	Posterior SD
250	12915.85	18523.12	8699.87
253	22747.87	23063.76	1535.53
262	20254.41	20506.36	2581.87
265	15846.22	16694.98	7601.15
269	20135.05	19975.15	4667.11
270	19931.96	19955.13	6033.35
956	19659.11	19795.60	1227.99
959	19159.69	13375.80	19256.94
961	18631.44	19498.31	7970.44

83-90

ρ

MCAT	Mean	Median	Posterior SD
245	0.65	0.65	0.014
250	0.51	0.51	0.002
253	0.47	0.47	0.010
259	0.75	0.75	0.009
262	0.41	0.41	0.001
269	0.57	0.57	0.046
270	0.74	0.75	0.027
663	0.51	0.51	0.001
667	0.49	0.49	0.022
956	0.43	0.43	0.003
959	0.55	0.55	0.004
960	0.45	0.45	0.004
961	0.59	0.59	0.001

v

MCAT	Mean	Median	Posterior SD
245	20211.82	20204.95	1276.83
250	236.03	192.53	134.67
253	20455.18	20140.50	1521.72
259	20246.14	20186.61	898.99
262	20445.49	20348.56	343.70
269	34386.49	25951.03	24030.32
270	20253.34	19908.07	9269.02
663	19563.87	19624.09	331.04
667	20089.55	20078.27	2723.34
956	20581.67	20664.71	913.92
959	19242.41	18707.09	5076.03
960	20059.66	20012.80	1703.89
961	20127.69	20141.04	580.80

- Degree of smoothing (heirarchical parameters, rho)
- Report mean/variance of example
- Add v and ρ tables across all runs

Discussion

Appendix
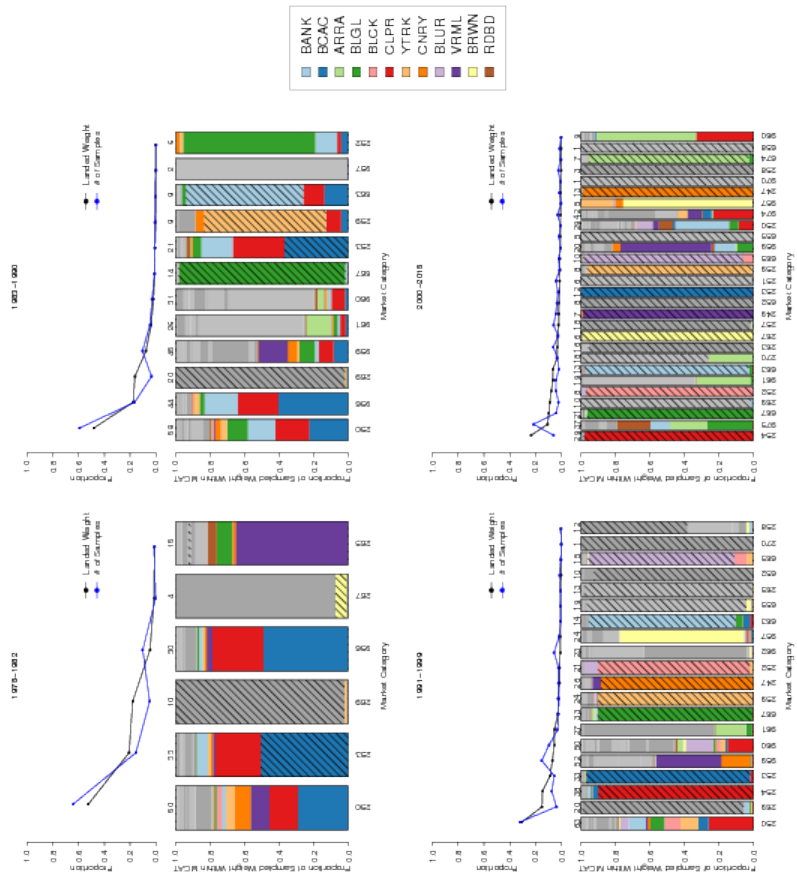
Discussion

- Variance Estimates; Justify Model based statistics
- Biase/Variance trade off; heirarchical modeling
- Model averaging
- Looking Forward
  - forcasting/hindcasting
    * simple
    * timeseries models
  - more computation faster
    * broader model exploration
    * broader spatial expansion
  - Heirarchical Spatial Models
  - DP Models

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