Revisiting Identifying Assumptions for Population Size Estimation

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Abstract

The problem of estimating the size of a population based on a subset of individuals observed across multiple data sources is often referred to as capture-recapture or multiple-systems estimation. This is fundamentally a missing data problem, where the number of unobserved individuals represents the missing data. As with any missing data problem, multiple-systems estimation requires users to make an untestable identifying assumption in order to estimate the population size from the observed data. Approaches to multiple-systems estimation often do not emphasize the role of the identifying assumption during model specification, which makes it difficult to decouple the specification of the model for the observed data from the identifying assumption. We present a re-framing of the multiple-systems estimation problem that decouples the specification of the observed-data model from the identifying assumptions, and discuss how log-linear models and the associated no-highest-order interaction assumption fit into this framing. We present an approach to computation in the Bayesian setting which takes advantage of existing software and facilitates various sensitivity analyses. We demonstrate our approach in a case study of estimating the number of civilian casualties in the Kosovo war. Code used to produce this manuscript is available at [https://github.com/aleshing/revisiting-identifying-assumptions](https://github.com/aleshing/revisiting-identifying-assumptions).

Keywords: Capture-recapture; Missing data; Multiple-systems estimation; Sensitivity analysis.
1 Introduction

Estimating the size of a closed population is a common problem in many fields, including ecology (Otis et al., 1978), epidemiology (Hook and Regal, 1995), official statistics (Anderson and Fienberg, 1999), and human rights (Ball et al., 2002). The available data typically take the form of multiple lists which record information on a subset of individuals in a population. When there exists a mechanism to identify which individuals are the same across lists, multiple-systems estimation (MSE), also known as capture-recapture, provides an approach to estimating the population size based on the overlap of the lists (Bird and King, 2018).

MSE is at its heart a missing data problem, as we do not observe all individuals in the population of interest (see e.g. Fienberg and Manrique-Vallier, 2009; Manrique-Vallier, 2016). As is the case in any missing data problem, MSE requires users to make an untestable identifying assumption about how the observed individuals relate to the unobserved individuals in order to estimate the population size from the observed data. We believe that this requirement is not sufficiently appreciated, as it is usually conflated with model specification, which involves both making an identifying assumption and specifying a model for the observed data. See for example Fienberg (1972) who wrote “... we are assuming that the model which describes the observed data also describes the count of the unobserved individuals. We have no way of checking this assumption,” and Manrique-Vallier et al. (2013) who wrote “The arguably most basic assumption in MSE is that the noninclusion of the fully unobserved individuals ... can be represented by the same model that represents the inclusion (and noninclusion) of those we can observe in at least one list. This is a strong and untestable condition.”

This conflation of identifying assumption specification and model specification has led practitioners to perform model evaluation by comparing a suite of model fits that are the results of both fundamentally different identifying assumptions and different model specifications for the observed data (see e.g. Sadinle, 2018; Manrique-Vallier et al., 2019; Silverman, 2020). This makes it essentially impossible to disentangle whether differences in inferences are due to differences in identifying assumptions, model specifications for the observed data, or some combination.

In this article, we propose a Bayesian approach to MSE that places the identifying assumption front and
center in the MSE workflow. We first revisit the framing of MSE as a missing data problem in Section 2. Section 3 reviews two common MSE models—log-linear and latent class models—through our missing data framing. In Section 4 we focus on the identifying assumption associated with log-linear models, and describe how it can be used as a building block for alternative identifying assumptions. In Section 5 we present an approach to computation in the Bayesian setting that allows us to use any identifying assumption in conjunction with any prior specification by taking advantage of existing software. This approach facilitates sensitivity analyses that examine the impact of both the prior and the identifying assumption. Finally, in Section 6 we illustrate our approach in a case study of estimating the number of civilian casualties in the Kosovo war.

2 Multiple-Systems Estimation as a Missing Data Problem

2.1 The Data

Suppose we have a closed population of $N$ individuals, of which $n < N$ are observed by one or more of $K$ lists. Let $H = \{0, 1\}^K$ denote the possible patterns of inclusion of the individuals in the lists, $H^* = H \setminus \{0\}^K$ denote the possible subsets of lists in which each of the $n$ observed individuals could have been observed, and let $x_i \in H$ denote the subset of lists in which individual $i$ was included. For example, with $K = 3$, $x_i = (0, 1, 1)$ indicates that individual $i$ was observed in lists 2 and 3, but not list 1.

These data for the $N$ individuals can be gathered into a $2^K$ contingency table of list overlap, where the cells of the table are indexed by $h \in H$, with counts $n_h = \sum_{i=1}^{N} I(x_i = h)$. We do not observe the count for cell $\{0\}^K$, $n_0 := n_{(0,\ldots,0)} = N - n$, which records the number of individuals missing from all lists, so the observed contingency table is incomplete. Let $n = \{n_h\}_{h \in H^*}$ denote the counts of the incomplete contingency table. The unobserved cell count $n_0$, or equivalently the population size $N$, is the target of inference.
2.2 The Complete-Data Distribution

Under independent and identically distributed (i.i.d.) sampling of individuals by the lists, the $2^K$ contingency table of counts is multinomially distributed, i.e.

$$n, n_0 \mid N, \pi \sim \text{Multinomial}(N, \pi),$$

where $\pi = \{\pi_h\}_{h \in H} \in \mathbb{S}^{2^K-1}$ is a set of cell probabilities, and $\mathbb{S}^d = \{(a_1, \cdots, a_{d+1}) \in \mathbb{R}^{d+1} \mid \sum_{i=1}^{d+1} a_i = 1, a_i > 0 \ \forall i\}$ denotes the $d$-dimensional probability simplex. We will refer to the model in (1) as the complete-data distribution, for which the evaluation relies on knowing the complete $2^K$ contingency table of counts. In general, the parameter space for this model will be some subset of $\Theta = \{N, \pi \mid N \in \mathbb{N}, \pi \in \mathbb{S}^{2^K-1}\}$, which we will refer to as the complete-data parameterization. As shown in Appendix A, when individuals are not i.i.d. sampled, but are sampled independently with cell probabilities drawn i.i.d. from some mixing distribution on $\mathbb{S}^{2^K-1}$, we also arrive at the model in (1). This is the case for common models for heterogeneity such as the $M_h$ and $M_{th}$ models of Otis et al. (1978).

2.3 Decomposing the Complete-Data Distribution

It is instructive to decompose the complete-data distribution as

$$p(n, n_0 \mid N, \pi) = N! \prod_{h \in H} \frac{n_h^{n_h}}{n_h!} = L_1(N, \pi_0 \mid n) L_2(\tilde{\pi} \mid n),$$

with $L_1(N, \pi_0 \mid n) = \binom{N}{n} \pi_0^{N-n} (1 - \pi_0)^n$ and $L_2(\tilde{\pi} \mid n) = n! \prod_{h \in H} \tilde{n}_h^{n_h} / n_h!$, where $\pi_0 := \pi_{(0, \cdots, 0)} = 1 - \sum_{h \in H} \pi_h$ is the probability of being missing from every list, and $\tilde{n}_h = \frac{n_h}{1 - \pi_0} = \sum_{h' \in H \setminus h} \pi_{h'}$ is the probability of being observed in the subset of the lists $h$ conditional on being observed in at least one list. $L_1$ is a binomial likelihood for $n$, which has been well studied in the related binomial $N$ problem literature (see e.g. Rukhin 1975). $L_2$ is a multinomial likelihood for the observed data $n$ conditional on their sum $n$, referred to as the conditional likelihood (Fienberg 1972). We will refer to $\pi_0$ as the unobserved cell probability and to $\tilde{\pi}$ as the observed cell probabilities. This decomposition hints at an alternative to the complete-data parameterization $\Theta, \Theta^* = \{N, \pi_0, \tilde{\pi} \mid N \in \mathbb{N}, \pi_0 \in (0, 1), \tilde{\pi} \in \mathbb{S}^{2^K-2}\}$, which we will refer to as the observed-data parameterization. The two parameterizations are equivalent, so we will work with whichever is more convenient for exposition.
2.4 Identifiability

Before performing inference in a statistical model, it is important to check that the model is identifiable. For $\theta \in \Theta^*$, let $P_{\theta}$ denote the complete-data distribution at the set of parameters $\theta$. Consider the following standard definition of identifiability:

**Definition 1.** The statistical model $\mathcal{P}_\Omega = \{P_{\theta} \mid \theta \in \Omega \subset \Theta^*\}$ is **identifiable** if $\forall \theta_1, \theta_2 \in \Omega$, $P_{\theta_1} = P_{\theta_2}$ implies that $\theta_1 = \theta_2$. Equivalently, $\mathcal{P}_\Omega$ is identifiable if $\forall \theta_1 = \{N, \pi_0, \hat{\pi}\}, \theta_2 = \{N', \pi'_0, \hat{\pi}'\} \in \Omega$, $L_1(N, \pi_0 \mid n)L_2(\hat{\pi} \mid n) = L_1(N', \pi'_0 \mid n)L_2(\hat{\pi}' \mid n) \forall n$ implies that $\theta_1 = \theta_2$.

One can show that the unrestricted model $\mathcal{P}_{\Theta^*}$ is identifiable. Since the goal is to estimate $N$, sufficiency might lead one to try to estimate $N$ and $\pi_0$ in the unrestricted model based solely on the binomial likelihood for $n$. Examining the likelihood surface for a given $n$, one finds a maximum at $N = n$ and $\pi_0 = 0$, with a ridge centered along the set $\{N \in \mathbb{N}, \pi_0 \in (0, 1) \mid N(1 - \pi_0) \approx n\}$ that monotonically decreases as $N$ increases. In Figure 1, we plot this surface when $n = 100$. There is a fundamental problem in that two parameters are being estimated with one data point, which makes it impossible to construct an unbiased or consistent estimator of either $N$ or $\pi_0$ [DasGupta and Rubin, 2005; Farcomeni and Tardella, 2012]. Thus the standard definition of identifiability is misleading in this setting, as it does not necessarily imply that the parameters are estimable in any traditional sense.

![Figure 1: Likelihood surface of $L_1$ when $n = 100$.](image-url)
We will instead use the following alternative definition of identifiability specific to MSE (Link, 2003; Holzmann et al., 2006):

**Definition 2.** The statistical model $P_\Omega$ is **conditionally identifiable** if $\forall \theta_1 = \{N, \pi_0, \tilde{\pi}\}, \theta_2 = \{N', \pi'_0, \tilde{\pi}'\} \in \Omega, L_2(\tilde{\pi} \mid n) = L_2(\tilde{\pi}' \mid n) \forall n$ implies that $\pi_0 = \pi'_0$.

In a conditionally identifiable model, the conditional likelihood, $L_2$, identifies the unobserved cell probability, $\pi_0$. Clearly the unrestricted model $P_{\Theta^\ast}$ is not conditionally identifiable. Standard identifiability of the multinomial conditional likelihood tells us that we can equivalently state Definition 2 as follows: the statistical model $P_\Omega$ is conditionally identifiable if $\forall \theta_1 = \{N, \pi_0, \tilde{\pi}\}, \theta_2 = \{N', \pi'_0, \tilde{\pi}'\} \in \Omega, \tilde{\pi} = \tilde{\pi}'$ implies that $\pi_0 = \pi'_0$. Thus for a conditionally identifiable model, there exists a function $T: \tilde{T} \rightarrow (0, 1)$ that maps observed cell probabilities, $\tilde{\pi}$, to unobserved cell probabilities, $\pi_0$, where $\tilde{T} \subset S^{2K-2}$. When the domain $\tilde{T}$ of this function is not equal to $S^{2K-2}$, this restricts the set of possible values for $\tilde{\pi}$ in the model to $\tilde{T}$. Any extra assumptions in the model involving $\tilde{\pi}$ can then further restrict the set of possible values for $\tilde{\pi}$ in the model to a set $\tilde{S} \subset \tilde{T}$. Thus conditionally identifiable models take the form $P_\Omega$, where $\Omega = \{N, \pi_0, \tilde{\pi} \mid N \in \mathbb{N}, \pi_0 = T(\tilde{\pi}), \tilde{\pi} \in \tilde{S}\}$.

When a model is not conditionally identifiable, we have no guarantees for when the parameters are estimable in any traditional sense. In particular, non-identifiability precludes consistent estimation as “there will be uncertainty in parameter estimates that is not washed out as more data are collected” (Linero, 2017). If a model $P_\Omega$ is conditionally identifiable, all parameters of the model can be consistently estimated (Sanathanan, 1972). However, we emphasize that the data needs to have been generated by a distribution in the model $P_\Omega$ for the parameters to be consistently estimable. In other words, in order to estimate the population size $N$, we need to assume a functional relationship, $T$, between the observed cell probabilities $\tilde{\pi}$ and the unobserved cell probability $\pi_0$. This is the main idea behind MSE.

### 2.5 Missing Data

The framing in the previous section is motivated by our treatment of MSE as a missing data problem. The decomposition in (2) is related to the decomposition in the missing data literature of the complete-data distribution into the **extrapolation distribution** and the **observed-data distribution** (Hogan and Daniels).
The extrapolation distribution captures how to extrapolate to the missing data given the observed data, which in our context corresponds to $L_1$. The observed-data distribution, as the name indicates, is the distribution of the observed data, which in this context corresponds to $L_2$. Following the analogy of the missing data literature, by restricting ourselves to models of the form $P_\Omega$, where $\Omega = \{N, \pi_0, \tilde{\pi} \mid N \in \mathbb{N}, \pi_0 = \mathcal{T}(\tilde{\pi}), \tilde{\pi} \in \tilde{S}\}$, one is making an identifying assumption, $\mathcal{T}$, about how $\tilde{\pi}$ relates to $\pi_0$ in order to identify $\pi_0$.

The observed-data distribution is restricted when the set of possible values for the observed cell probabilities, $\tilde{S}$, is not equal to $\mathbb{S}^{2^K-2}$. Based on standard properties of the multinomial conditional likelihood, restrictions on the observed-data distribution are assumptions that are testable from the data. As noted in the previous section, these restrictions could be due to the domain, $\tilde{T}$, of the identifying assumption (see Section 4.3 for an example), or due to extra modeling assumptions for the observed cell probabilities, $\tilde{\pi}$ (see Section 3.1 for an example). When the observed-data distribution is not restricted by the model, i.e. $\tilde{S} = \tilde{T} = \mathbb{S}^{2^K-2}$, we refer to the model as nonparametric identified (see Chapter 8 of Hogan and Daniels [2008]).

In the MSE literature, previous work has been concerned with determining when certain models are conditionally identified (see e.g. Link et al. 2003; Holzmann et al. 2006). Here we are concerned with determining both when and how models are conditionally identified. Since the validity of our inferences rests on the untestable identifying assumption and any restrictions on the observed-data distribution being correct, we would like to know what identifying assumption we are actually making so we can determine whether or not the assumption is plausible in a given context. Thus, in this article we will advocate for the use of models based on explicit identifying assumptions, where the observed-data distribution is only possibly restricted by the identifying assumption (i.e. $\tilde{S} = \tilde{T}$), so that we make as few testable assumptions as possible.

### 3 Log-Linear and Latent Class Models

In this section we describe two commonly used models, which we use to demonstrate the drawbacks of using models that either place unnecessary restrictions on the observed-data distribution or are not based on explicit identifying assumptions.
3.1 Log-Linear Models

Any set of cell probabilities, $\pi \in \mathbb{S}^{2K-1}$, can be represented as $\pi_h = \mu_h / \sum_{h' \in H} \mu_{h'}$, where $\log(\mu_h) = \sum_{h' \in H'} \lambda_{h'} \prod_{k=1}^K h_k', h_k' \in H, h_k \in \{0, 1\}$, for some set of log-linear parameters $\lambda = \{\lambda_h\}_{h \in H^*} \in \mathbb{R}^{2K-1}$. This leads to the log-linear parameterization $\Theta_{LL} = \{N, \lambda \mid N \in \mathbb{N}, \lambda \in \mathbb{R}^{2K-1}\}$. For cells in the incomplete table $h \in H^*$ such that $\sum_{k=1}^K h_k = 1$ we refer to $\lambda_h$ as a main effect; for $h \in H^*$ such that $\sum_{k=1}^K h_k = \ell > 1$ we refer to $\lambda_h$ as an $\ell$-way interaction. The main effects and interactions all have interpretations as log ratios of certain cross-product ratios (see e.g. Chapter 2 of Bishop et al., 1975). Of particular interest is the $K$-way, or highest-order, interaction $\lambda_1$, where $\mathbf{1} := (1, \cdots, 1)$, for which we have the relationship $\prod_{h \in H} \pi_{h}^{I_{\text{odd}}(h)} / \prod_{h \in H} \pi_{h}^{I_{\text{even}}(h)} = \exp\{(-1)^{I_{\text{even}}(1)} \lambda_1\}$, where $I_{\text{odd}}(h) = I(\sum_{k=1}^K 2 - h_k \text{ is odd})$ and $I_{\text{even}}(h) = I(\sum_{k=1}^K 2 - h_k \text{ is even})$. This notation differs from Bishop et al. (1975) as we index the complete table by $H = \{0, 1\}^K$ rather than $\{2, 1\}^K$.

The model $\mathcal{P}_{\Theta_{LL}}$ is equivalent to the unrestricted model $\mathcal{P}_\Theta$, so we need to restrict $\Theta_{LL}$ to identify the unobserved cell probability $\pi_0$. It is standard in this scenario to set $\lambda_1 = 0$, so that there is no highest-order interaction in the model. Referring to the resulting parameter space as $\Omega_{LL}$, we would like to understand the identifying assumption made by the saturated model $\mathcal{P}_{\Omega_{LL}}$. In Appendix B, we show $\mathcal{P}_{\Omega_{LL}}$ is nonparametric identified and that this no-highest-order interaction (NHOI) assumption corresponds to the explicit identifying assumption $T(\tilde{\pi}) = (\tilde{\Pi}_{\text{odd}} / \tilde{\Pi}_{\text{even}}) / (1 + \tilde{\Pi}_{\text{odd}} / \tilde{\Pi}_{\text{even}})$, where $\tilde{\Pi}_{\text{odd}} = \prod_{h \in H^*} \tilde{\pi}_{h}^{I_{\text{odd}}(h)}$ and $\tilde{\Pi}_{\text{even}} = \prod_{h \in H^*} \tilde{\pi}_{h}^{I_{\text{even}}(h)}$, which we discuss in more detail in Section 4.

In practice there is an emphasis on achieving low variance estimates of the log-linear parameters and, consequently, $N$. To this end, rather than just setting the highest-order interaction to zero and using the saturated model, it is common to further restrict the model and set other interactions to zero. This is the case, for example, when restricting to decomposable graphical models (Madigan and York, 1997), or when only including main effects and 2-way interactions (Silverman, 2020), which can be hard to justify in practice (see e.g. Dellaportas and Forster, 1999; Whitehead et al., 2019). By restricting the observed-data distribution, we are making a testable assumption that, in addition to the untestable identifying assumption, must be correct in order for inferences to be valid. The hope is that by specifying a model with fewer parameters, the resulting estimates will have lower variance if the chosen restricted model generated the data. However,
if the chosen restricted model did not generate the data, estimates of $N$ can be arbitrarily biased, and more generally can have arbitrarily poor frequentist properties (Regal and Hook [1991]; Whitehead et al. [2019]).

This is a classic bias-variance trade off, which has been acknowledged since the seminal work of Fienberg (1972) (edited to match our notation): “In analyzing multiple recapture census data our aim is to fit the incomplete $2^K$ table by a log linear model with the fewest possible parameters, since the fewer parameters in an ‘appropriate’ model for estimating $n_0$, the smaller the variance of the estimate. Thus it is not a good practice simply to use the saturated model. On the other hand, if we use a model with too few parameters, we introduce a bias into our estimate of population size that can possibly render the variance formulae of the next section meaningless.” We disagree with Fienberg (1972) in that we believe there is a clear route to take in this case: make as few testable assumptions as possible (i.e. use the saturated model $\mathcal{P}_{\Omega_{LM}}$) in the hopes of not being arbitrarily biased. Some form of regularization can then be used within the saturated model $\mathcal{P}_{\Omega_{LM}}$ in order to produce lower variance estimators, e.g. through priors in a Bayesian framework as discussed in Section 5.1.

3.2 Latent Class models

Latent class models (LCMs) are typically motivated as models of multivariate categorical data that capture individual heterogeneity when the population can be stratified into $J$ classes, where lists sample individuals independently within each class (Haberman [1979]; Manrique-Vallier, 2016). Thus they are so-called $M_{th}$ models as described in Appendix A (Otis et al., 1978). Corollary 1 of Dunson and Xing (2009) shows that for any set of cell probabilities $\pi \in \mathbb{S}^{2^K-1}$, there exists some $J < \infty$ such that $\pi$ can be represented as a $J$-class latent class model, i.e. $\pi_h = \sum_{j=1}^J \nu_j \prod_{k=1}^K q_{jk}^{h_k}(1-q_{jk})^{1-h_k}$, where $\nu = (\nu_1, \cdots, \nu_J)$ are class membership probabilities, and $q = \{q_{jk}\}_{j=1,k=1}^{J,K}$ are class specific observation probabilities for each list. This leads to the latent class model parameterization $\Theta_{LCM} = \{N, \nu, q, J \mid N \in \mathbb{N}, \nu \in \mathbb{S}^{J-1}, q \in (0,1)^{J \times K}, J \in \mathbb{N}\}$. As $\mathcal{P}_{\Theta_{LCM}}$ is equivalent to the unrestricted model $\mathcal{P}_\Theta$, we need to restrict $\Theta_{LCM}$ to identify the unobserved cell probability $\pi_0$. It is common to fix the number of latent classes, $J$, in advance, to arrive at the the restricted parameterization $\Omega_{LCM,J} = \{N, \nu, q \mid N \in \mathbb{N}, \nu \in \mathbb{S}^{J-1}, q \in (0,1)^{J \times K}\}$.

In Appendix A we show that $\mathcal{P}_{\Omega_{LCM,J}}$ is conditionally identified if and only if $2J \leq K$. However, when
\(\mathcal{P}_{\Omega_{\text{LCM},J}}\) is conditionally identified we do not know what explicit identifying assumption is being made or whether the model is nonparametric identified. A recent development in MSE is the use of LCMs with \(J\) large enough that \(2J > K\) (Manrique-Vallier, 2016). Here LCMs suffer from the opposite problem of log-linear models: rather than making too many assumptions, and hence restricting the observed-data distribution, so few assumptions are being made that the model is not conditionally identified. In Appendix C we show through a variety simulations that this is a practically relevant problem, as we have no guarantees for when estimates based on non-identified models are going to be accurate.

4 Revisiting Log-Linear Models and Their Identifying Assumptions

In this section we revisit the NHOI identifying assumption associated with log-linear models and discuss its role in our framing of MSE. We then describe how this assumption can be used as a building block for alternative identifying assumptions.

4.1 The No-Highest-Order Interaction Assumption

The NHOI assumption introduced in Section 3.1 can be interpreted as follows: for any given subset of \(K - 1\) lists, appearing in all \(K - 1\) lists is not associated with appearing or not appearing in the \(K\)th list. Here the meaning of “associated with” changes as the number of lists \(K\) changes. When \(K = 2\) we are assuming that the odds of appearing in list 1 conditional on appearing in list 2 is equal to the odds of appearing in list 1 conditional on not appearing in list 2, and thus the lists are independent: 

\[
\pi_{(1,0)}/\pi_{(0,0)} = \pi_{(1,1)}/\pi_{(0,1)}.
\]

When \(K = 3\) we are assuming that the odds ratio for lists 1 and 2 conditional on appearing in list 3 is equal to the odds ratio for lists 1 and 2 conditional on not appearing in list 3: 

\[
\pi_{(1,1,1)}/\pi_{(0,0,1)} = \pi_{(1,1,0)}/\pi_{(0,0,0)} = \pi_{(1,1,0)}/\pi_{(0,0,0)}.
\]

When \(K = 4\) we assume that certain ratios of odds ratios are equal, and so on for larger \(K\).

As discussed in Section 2.5 in order to use the NHOI assumption in a given application, we need to be able to determine whether or not it is plausible. Odds and odds ratios are well understood in statistics...
(Bishop et al., 1975), and thus the NHOI assumption may be of use when there are $K = 2$ or $K = 3$ lists. However, higher order measures of association like ratios of odds ratio are more obscure and hard to interpret, which makes the NHOI assumption difficult to use when there are more than $K = 3$ lists. This difficulty compounds when considering sensitivity analyses as we explain in the next section.

### 4.2 Sensitivity Analyses for the No-Highest-Order Interaction Assumption

Sensitivity analyses aim to gauge how sensitive inferences are to untestable assumptions, and are an important part of missing data workflows (see Chapter 9 of Hogan and Daniels, 2008). The NHOI assumption facilitates sensitivity analyses based on varying the highest-order interaction across a range of non-zero values. In particular, when fixing $\xi = \exp\{(-1)^{I_{\text{even}}(1)} \lambda_1\} \in \mathbb{R}^+$, we show in Appendix B that we arrive at the explicit identifying assumption $T(\tilde{\pi}) = (\tilde{\Pi}_{\text{odd}}/\tilde{\Pi}_{\text{even}})/(\xi + \tilde{\Pi}_{\text{odd}}/\tilde{\Pi}_{\text{even}})$. This generalizes the two list sensitivity analyses of Lum and Ball (2015) and Gerritse et al. (2015). Under this identifying assumption, rather than assuming certain measures of association are equal, we are assuming one measure is $\xi$ times another. For example, when $K = 2$ we are assuming that the odds of appearing in list 1 conditional on not appearing in list 2 is $\xi$ times the odds of appearing in list 1 conditional on appearing in list 2: $\pi_{(1,0)}/\pi_{(0,0)} = \xi \pi_{(1,1)}/\pi_{(0,1)}$.

In order to perform a meaningful sensitivity analysis, one needs to be able to specify a range of values for the highest-order interaction that are plausible for a given application. Due to our understanding of odds and odds ratios, performing this sort of sensitivity analysis may be possible when there are $K = 2$ or $K = 3$ lists. When considering more than $K = 3$ lists, it can become difficult to even start thinking about whether it is plausible that $\xi$ is less than or greater than 1, let alone determine specific values of $\xi$ that are plausible.

### 4.3 $K'$-List Marginal No-Highest-Order Interaction Assumptions

The NHOI assumption can be used as a building block to generate other identifying assumptions. Suppose we can assume that, without loss of generality, the NHOI assumption holds for the first $1 < K' < K$ lists, marginal of the remaining $K - K'$ lists. This leads to a new identifying assumption which in general does not imply that there is no highest-order interaction for all $K$ lists. To introduce this assumption formally we need to introduce some notation. Let $G = \{0, 1\}^{K'}$ index the marginal $2^{K'}$ contingency table for the
first $K'$ lists and $G^* = G \setminus \{0\}^{K'}$. For a set of cell probabilities, $\pi \in S^{2^K-1}$, and a given cell in the marginal table, $g \in G$, let $\pi_{g+} = \sum_{h \in H} \pi_h I\{(h_1, \ldots, h_{K'}) = g\}$ denote the probability of being observed in cell $g$ of the marginal table implied by $\pi$. Similarly let $\tilde{\pi}_{g+} = \sum_{h \in H} \tilde{\pi}_h I\{(h_1, \ldots, h_{K'}) = g\}$ and $\tilde{\pi}_{0+} = \sum_{h \in H} \tilde{\pi}_h I\{(h_1, \ldots, h_{K'}) = (0, \ldots, 0)\}$.

Assuming that the NHOI assumption holds for the first $1 < K' < K$ lists, marginal of the remaining $K - K'$ lists, is equivalent to assuming $\prod_{g \in G} \pi_{g+}^{I_{\text{odd}}(g)} / \prod_{g \in G} \pi_{g+}^{I_{\text{even}}(g)} = 1$. In Appendix B we show that this $K'$-list marginal no-highest-order interaction assumption corresponds to the explicit identifying assumption $T(\tilde{\pi}) = (\tilde{\Pi}_{\text{odd},+}/\tilde{\Pi}_{\text{even},+} - \tilde{\pi}_{0+})/(1 + \tilde{\Pi}_{\text{odd},+}/\tilde{\Pi}_{\text{even},+} - \tilde{\pi}_{0+})$, where $\tilde{\Pi}_{\text{odd},+} = \prod_{g \in G^*} \pi_{g+}^{I_{\text{odd}}(g)}$ and $\tilde{\Pi}_{\text{even},+} = \prod_{g \in G^*} \pi_{g+}^{I_{\text{even}}(g)}$. Further, we can perform sensitivity analyses for this assumption by fixing $\prod_{g \in G} \pi_{g+}^{I_{\text{odd}}(g)} / \prod_{g \in G} \pi_{g+}^{I_{\text{even}}(g)} = \xi \in \mathbb{R}^+$. As we show in Appendix B, this leads to the explicit identifying assumption

$$
T(\tilde{\pi}) = \frac{\tilde{\Pi}_{\text{odd},+}/\tilde{\Pi}_{\text{even},+} - \xi \tilde{\pi}_{0+}}{\xi + (\tilde{\Pi}_{\text{odd},+}/\tilde{\Pi}_{\text{even},+} - \xi \tilde{\pi}_{0+}).}
$$

Models that use the assumption that $\prod_{g \in G} \pi_{g+}^{I_{\text{odd}}(g)} / \prod_{g \in G} \pi_{g+}^{I_{\text{even}}(g)} = \xi \in \mathbb{R}^+$ are not nonparametric identified, as the domain of the identifying assumption is $\tilde{T} = \{\tilde{\pi} \in S^{2^K-2} \mid \tilde{\Pi}_{\text{odd},+}/(\tilde{\Pi}_{\text{even},+} \tilde{\pi}_{0+}) > \xi\}$.

A special case of this identifying assumption was originally suggested in [Regal and Hook (1998)] as an alternative to the NHOI assumption. They considered a data set consisting of $K = 3$ lists recording cases of spina bifida in upstate New York, where they believed that the assumption that two of the lists were marginally independent (i.e., using the 2-list marginal NHOI assumption) was more plausible than the NHOI assumption. This illustrates that there may be applications where one may be more willing to make marginal assumptions about a subset of $K'$ lists, rather than an assumption involving all $K$ lists. Additionally when there are $K > 3$ lists and $K' = 2$ or $K' = 3$, the $K'$-list marginal NHOI assumption and its sensitivity analyses are much more straightforward to interpret than the highest-order interaction and its sensitivity analyses, as discussed in Sections 4.1 and 4.2.

For these reasons, we believe that the $K'$-list marginal NHOI assumption can be useful as an explicit identifying assumption in the toolbox of the MSE practitioner. However, we emphasize that there is no one-size-fits-all identifying assumption. Specification of identifying assumptions in practice should be accompanied with appropriate justification based on the context of the data. In Section 6.1 we attempt to
provide such a justification for our use of the 2-list marginal NHOI assumption in an application estimating the number of civilian casualties in the Kosovo war.

5 Computation for Bayesian Multiple-Systems Estimation

In this section we describe a computational approach that allows any identifying assumption to be used in a Bayesian framework with any prior for the population size, \( N \), and any prior for the observed cell probabilities, \( \tilde{\pi} \). Various sensitivity analyses are facilitated from this approach. We further give some guidance to specification of the prior for \( N \).

5.1 Bayesian Multiple-Systems Estimation

Suppose that we are using a conditionally identified model \( \mathcal{P}_\Omega \), where \( \Omega = \{ N, \pi_0, \tilde{\pi} \mid N \in \mathbb{N}, \pi_0 = \mathcal{T}(\tilde{\pi}), \tilde{\pi} \in \tilde{S} \} \), and we have specified independent prior distributions for \( N \) and \( \tilde{\pi} \). The posterior distribution of \( N \) and \( \tilde{\pi} \) is

\[
p(\tilde{\pi} \mid n, \pi_0) = \frac{L_1(N, \pi_0 \mid n)p(N)p(\tilde{\pi})I(\tilde{\pi} \in \tilde{S})}{\sum_{N=1}^{\infty} L_1(N, \pi_0 \mid n)p(N)p(\tilde{\pi})I(\tilde{\pi} \in \tilde{S})},
\]

and

\[
p(n \mid \pi_0) = \int p(n \mid \mathcal{T}(\tilde{\pi}))p(\tilde{\pi} \mid \pi_0)d\tilde{\pi},
\]

where \( p(n \mid \pi_0) = \sum_{N=1}^{\infty} L_1(N, \pi_0 \mid n)p(N) \) and \( p(N \mid n, \pi_0) = L_1(N, \pi_0 \mid n)p(N)/p(n \mid \pi_0) \), with \( \pi_0 = \mathcal{T}(\tilde{\pi}) \). As we discuss in Section 5.3, we can compute \( p(n \mid \pi_0) \), and thus \( p(N \mid n, \pi_0) \), analytically for common priors on \( N \). If one has access to Markov chain Monte Carlo (MCMC) samples \( \{ \tilde{\pi}[i] \}_{i=1}^{T} \) from \( p(\tilde{\pi} \mid n) \), one can then generate MCMC samples \( \{ N[i] \}_{i=1}^{T} \) from \( p(N \mid n) \) via \( N[i] \sim p(N \mid n, \mathcal{T}(\tilde{\pi}[i])) \). Summaries of the marginal posterior of \( N \) can then be calculated based on these samples.

5.2 Mixing and Matching Identifying Assumptions and Priors

While computation as described in the previous section may seem straightforward, the marginal posterior \( p(\tilde{\pi} \mid n) \) depends on the specific combination of priors for \( \tilde{\pi} \) and \( N \) and identifying assumption \( \mathcal{T} \). Thus we need new MCMC samples from \( p(\tilde{\pi} \mid n) \) for each new combination of priors and identifying assumption, which can be difficult both technically and computationally. Rather than develop new MCMC samplers for
each combination, we will rely on a combination of existing software and a computationally cheap rejection sampler.

Letting \( p_C(\tilde{\pi} \mid n) \propto L_2(\tilde{\pi} \mid n)p(\tilde{\pi}) \) denote the marginal posterior for \( \tilde{\pi} \) using just the conditional likelihood \( L_2 \), we can rewrite (1) as
\[
p\left(\tilde{\pi} \mid n_0\right) \propto p\left(n \mid T(\tilde{\pi}) \right)I(\tilde{\pi} \in \tilde{S})p_C(\tilde{\pi} \mid n).
\]
This suggests a computationally cheap rejection sampler to generate samples from \( p(\tilde{\pi} \mid n) \), if we have access to MCMC samples from \( p_C(\tilde{\pi} \mid n) \) (Smith and Gelfand, 1992):

1. Generate \( U \sim \text{Unif}(0, 1) \) and \( \tilde{\pi} \sim p_C(\tilde{\pi} \mid n) \) independently.

2. If \( U < p(n \mid T(\tilde{\pi}))I(\tilde{\pi} \in \tilde{S})/\{\max_{\pi_0} p(n \mid \pi_0)\} \) accept \( \tilde{\pi} \). Else go back to (1).

Thus, for a given prior \( p(\tilde{\pi}) \), if we want to perform prior sensitivity analyses for \( N \) and/or sensitivity analyses probing the identifying assumption as discussed in Section 4.2, we can take a one time sample from \( p_C(\tilde{\pi} \mid n) \) (see Table 1). Thus if we want to use the prior \( p(\tilde{\pi}) \) induced by a working prior \( p^w(\pi) \), we can rely on a combination of existing software and a computationally cheap rejection sampler to generate draws from the posterior \( p(N, \tilde{\pi} \mid n) \) for any combination of prior for \( N \) and identifying assumptions, as long as the software uses the prior \( p^w(N) \propto 1/N \). Note that our prior for \( N \) does not have to be \( p^w(N) \). This is the case for most existing software, including the R package conting (Overstall and King, 2014), which implements a reversible-jump MCMC sampler to target \( p^w(\pi \mid n) \) under a working prior \( p^w(\pi) \) induced by a prior that averages over
all hierarchical log-linear models (King and Brooks, 2001), and the R package LCMCR, which implements a 
data augmentation Gibbs sampler to target $p^w(\pi \mid n)$ under a working prior $p^w(\pi)$ induced by a Dirichlet 
process prior for LCMs (Manrique-Vallier, 2016). The steps of the MCMC samplers used in these packages 
are model specific and we would not be able to use them if we tried to create bespoke MCMC samplers 
targeting the marginal posterior in (4). We note that this approach is closely related to the working prior 
approach of Linero (2017), with some necessary modifications specific to MSE.

5.3 Recommended Priors for the Population Size, $N$

In Table 1 we catalog $p(n \mid \pi_0)$ and $p(N \mid n, \pi_0)$ under Poisson, negative-binomial, and binomial priors for $N$, in addition to the class of priors $p(N) \propto (N - \ell)!/N!$, where $\ell \in \{0, 1, 2, \cdots \}$, suggested by Fienberg et al. (1999). This class of priors contains both the improper uniform prior, $p(N) \propto 1$, when $\ell = 0$, and the improper scale prior, $p(N) \propto 1/N$, when $\ell = 1$. If $p(n \mid \pi_0)$ is not available analytically, for example when $p(N)$ is beta-binomial, we recommend truncating the prior for $N$ to the range $\{1, \cdots, N_{max}\}$ where $N_{max}$ is an upper bound on the population size, in which case $p(n \mid \pi_0)$ can be computed numerically.

Table 1: Catalog of $p(N \mid n, \pi_0)$ and $p(n \mid \pi_0)$ under common priors for $N$.

| Prior                  | $p(N)$                     | $p(N \mid n, \pi_0)$ | $p(n \mid \pi_0)$  |
|------------------------|----------------------------|-----------------------|---------------------|
| Pois$(M)$              | $(M)^N e^{-M}/N!$          | $n + \text{Pois}(\pi_0 M)$ | Pois$((1 - \pi_0)M)$ |
| NB $(a, \frac{M}{M+a})$| $(\frac{N+a-1}{N})^{M}(\frac{a}{M+a})^a$ | $n + \text{NB} \left(n + a \frac{M\pi_0}{M+a}\right)$ | NB $(a, \frac{(1-\pi_0)M}{1-(1-\pi_0)a})$ |
| Bin$(M, q)$            | $(\frac{M}{N}) q^N (1-q)^{M-N}$ | $n + \text{Bin} \left(M - n, \frac{\pi_0 q}{\pi_0 q + 1 - q}\right)$ | Bin$(M, (1-\pi_0)q)$ |
| Fienberg et al. (1999) | $\propto (N - \ell)!/N!$  | $n + \text{NB}(n - \ell + 1, \pi_0)$ | $\propto \frac{(n-\ell)!}{n!}(1 - \pi_0)^{\ell-1}$ |

The improper scale prior, under which $p(\hat{\pi} \mid n) \propto p_C(\hat{\pi} \mid n) I(\hat{\pi} \in \hat{S})$, is a common “noninformative” prior for $N$ and has the nice property that the posterior mean of $N$ conditional on $\hat{\pi}$ is the Horvitz-Thompson estimator (Horvitz and Thompson 1952), $n/(1 - T(\hat{\pi}))$, which is well understood in the present context (see e.g. Rukhin 1975). Following Link (2013), we recommend using this prior in the absence of substantive knowledge about $N$.

When incorporating substantive knowledge about $N$ into an informative prior for $N$ we recommend
using a negative-binomial or beta-binomial prior, as we have found Poisson and binomial priors to be more informative than we would usually like to use. For concreteness in this article we will focus on the negative-binomial prior. In Table 1 we use a common parameterization for the negative-binomial distribution in terms of the mean $M$ and overdispersion parameter $a$. This parameterization arises from a Poisson-gamma mixture, where $N \mid \delta \sim \text{Poisson}(M\delta), \delta \sim \text{Gamma}(a,a)$. As $a \to \infty$ the prior approaches a Poisson prior with mean $M$, and as $a \to 0$ the prior approaches the improper scale prior.

### 6 Civilian Casualties in the Kosovo War

In this section we estimate the number of civilian casualties in the Kosovo war between March 20 and June 22, 1999, using data originally analyzed in Ball et al. (2002). The data consist of $K = 4$ lists with $n = 4400$ observed casualties, and are presented in Table 2, reproduced from Section 6 of Ball et al. (2002). Three of the lists were constructed from refugee interviews conducted separately by the American Bar Association Central and East European Law Initiative (ABA), Human Rights Watch (HRW), and the Organization for Security and Cooperation in Europe (OSCE). The fourth list was constructed from exhumation reports conducted on behalf of the International Criminal Tribunal for the Former Yugoslavia (EXH). We refer the reader to Appendix 1 of Ball et al. (2002) for a detailed description of each list.

|       | ABA | yes | yes | no | no |
|-------|-----|-----|-----|----|----|
|       | EXH |     |     |    |    |
|       |     | yes | no  | yes| no |
|       | HRW | OSCE|     |    |    |
| yes   | yes | 27  | 32  | 42 | 123|
| yes   | no  | 18  | 31  | 106| 306|
| no    | yes | 181 | 217 | 228| 936|
| no    | no  | 177 | 845 | 1131| $n_0$|

After motivating our choice of identifying assumption in the next section, we will analyze the Kosovo data under a variety of priors for the population size and observed cell probabilities. Our purpose is to
demonstrate the ease with which it is possible to perform inference in a model with explicit identifying assumptions and arbitrary priors, as described in Section 5.2. This facilitates prior sensitivity analyses that decouple the identifying assumption from the model used for the observed cell probabilities. Since the same identifying assumption is being used for each prior combination, it follows that differences in fits are entirely due to differences in prior specifications. Compare this, for example, to the analyses of the Kosovo data set in Silverman (2020), where the Bayesian LCM of Manrique-Vallier (2016) was compared to various Bayesian log-linear models. The fits of these different models are not comparable to each other, as they are using different identifying assumptions and different priors for the observed cell probabilities. Note that we are not attempting to perform model selection or provide guidance on which prior specification one should use.

6.1 Choice of Identifying Assumption

For our main analysis, we will use the 2-list marginal NHOI assumption, where we will assume that the ABA and HRW lists are independent. We believe this assumption is plausible given that “there were no overt efforts by any of the researchers to exclude or include witnesses who had participated in another data collection project” (ABA/AAAS 2000, p. 40) and that the two lists had similarly extensive geographic reach in their interviews. In particular, ABA conducted interviews in Albania, Macedonia, Kosovo, the United States, and Poland, while HRW conducted interviews in Albania, Macedonia, Kosovo, and Montenegro. ABA only conducted around 10% of its interviews in the United States and Poland, and HRW only conducted 3% of its interviews in Montenegro. Further, within Kosovo, ABA and HRW conducted interviews in similar geographic regions. For more information on where the lists conducted interviews see Appendix 1 of Ball et al. (2002).

The original analysis of the Kosovo data set in Ball et al. (2002) used the NHOI assumption. To justify this assumption for the Kosovo data, as we have $K = 4$ lists, we would need to reason about certain ratios of odds ratios being equal, which can be difficult, as discussed in Section 4.1 and further explained in Appendix D. Nevertheless, to further demonstrate the use of the computational approach described in Section 5.2 in Appendix D we present an analysis of the Kosovo data using the NHOI assumption.
6.2 Priors for Total Number of Casualties

We will consider two priors for the total number of casualties, $N$, as discussed in Section 5.3: the improper scale prior and a negative-binomial prior. To inform the negative-binomial prior, we will rely on two studies that attempted to estimate the number of casualties in the Kosovo war using different data sources than Ball et al. (2002). Spiegel and Salama (2000) estimated there were 12000 casualties with a 95% confidence interval of [5500, 18300]. Iacopino et al. (2001) estimated there were 8000 casualties with a 95% confidence interval of [5800, 10200]. Using the negative-binomial parameterization given in Table 1, we will use a specification with mean $M = 10000$ (the average of the estimates from the two studies) and overdispersion parameter $a = 1.6$, which places 95% of the prior mass on [818, 30371]. This specification is meant to be weakly informative in the sense that the information it incorporates is intentionally weaker than what is available to us, so as to provide a proper alternative to the “noninformative” improper scale prior (see e.g. Gelman et al. 2017).

6.3 Priors for Observed Cell Probabilities

We will consider four prior specifications for the observed cell probabilities $\tilde{\pi}$: 1) a flat Dirichlet prior, i.e. $\tilde{\pi} \sim \text{Dirichlet}(1, \cdots, 1)$, under which $p_C(\tilde{\pi} \mid n)$ is available in closed form, 2) the prior induced from using $\text{Normal}(0, 5^2)$ priors for the log-linear parameters in the saturated log-linear model $\Omega_{LL}$, fit using the Stan probabilistic programming language (Carpenter et al. 2017), 3) the prior induced from using the Dirichlet process prior of Manrique-Vallier (2016) for the $J$ class LCM $\Omega_{LCM,J}$, with $J = 10$ and default hyperparameters, as implemented in the R package LCMCR, and 4) the prior induced from using the Bayesian model averaging prior of King and Brooks (2001) for the log-linear parameters in the saturated log-linear model $\Omega_{LL}$, with the unit information prior on log-linear parameters, as implemented in the R package conting (Overstall and King 2014). We note that conting uses an alternative log-linear parameterization based on sum to zero constraints rather than corner point constraints used in Section 3.1.

6.4 Main Analysis

For each combination of prior for $N$ and $\tilde{\pi}$ we fit the corresponding model using the computational approach described in Section 5.2. In particular, we emphasize that for each prior for $\tilde{\pi}$, we only drew samples from
the corresponding $p_C(\hat{\pi} \mid n)$ once. The posterior density for $N$ under each prior combination is displayed in Figure 2. Posterior means and 95% credible intervals for $N$ under each prior combination are displayed in Table 3. Assuming independence of the ABA and HRW lists, under the negative-binomial prior for $N$ and LCM prior for $\hat{\pi}$ of Manrique-Vallier (2016), we estimate there were 9359 civilian casualties, with a 95% credible interval of [7967, 11059]. This credible interval includes the point estimate from Iacopino et al. (2001), but not from Spiegel and Salama (2000).

![Prior for N](image.png)

Figure 2: Posterior density of $N$ under each combination of prior for $N$ and $\hat{\pi}$, using the marginal no-highest-order interaction assumption.

| Prior for N | Improper Scale Prior | Negative-Binomial |
|-------------|----------------------|-------------------|
| Dirichlet   | 9536 [8113, 11252]   | 9540 [8123, 11247]|
| Log-Linear  | 9764 [8277, 11549]   | 9766 [8288, 11550]|
| LCMCR       | 9353 [7959, 11063]   | 9359 [7967, 11059]|
| Conting     | 9618 [8224, 11195]   | 9621 [8232, 11191]|

Table 3: Posterior means and 95% credible intervals for $N$ under each combination of prior for $N$ and $\hat{\pi}$, using the marginal no-highest-order interaction assumption.

When using the LCM prior for $\hat{\pi}$, the posterior distribution for $N$ is not sensitive to our choice of prior.
for $N$, as it is essentially the same as when using the “noninformative” improper scale prior for $N$ instead of the negative-binomial prior. When considering the other priors for $\pi$, the posterior is again not sensitive to the prior for $N$. Across the different priors for $\pi$, the posterior summaries are fairly consistent, with the posterior summaries under the LCM prior for $\pi$ being slightly lower than under the other priors. We note that all of the credible intervals fall within the confidence interval of Spiegel and Salama (2000).

### 6.5 A Sensitivity Analysis Probing the Identifying Assumption

While we believe that it is plausible that the ABA and HRW lists are independent, we would also like to understand how sensitive our resulting estimates are to realistic violations of the assumption. If independence was violated, it would likely be the case that the lists are positively dependent and thus population size estimates under independence are downward biased, as is common in human rights applications (see e.g. the discussion in Section 5 of Lum and Ball, 2015). In particular, HRW selected regions in Kosovo to conduct interviews based on reports of human rights violations from refugees and other sources (ABA/AAAS, 2000). Thus it seems possible that a casualty appearing in HRW could be more likely to appear in ABA than a casualty that did not appear in HRW.

We now perform a sensitivity analysis probing the 2-list marginal NHOI assumption, focusing on the LCM prior for $\pi$ of Manrique-Vallier (2016) and the negative-binomial prior for $N$, for concreteness. We fit the model with the identifying assumption, varying $\xi$ over $\{0.7, 0.8, 0.9, 1\}$, using the computational approach described in Section 5.2. Thus in each case we are assuming that the odds of appearing in ABA conditional on not appearing in HRW is $\xi$ times the odds of appearing in ABA conditional on appearing in HRW. We emphasize that we only drew samples from $p_C(\hat{\pi} | n)$ under the LCM prior for $\pi$ of Manrique-Vallier (2016) once for both the main analysis in the previous section and the sensitivity analysis described now. The posterior density for $N$ under each identifying assumption is displayed in Figure 3. Posterior means and 95% credible intervals for $N$ under each identifying assumption combination are displayed in Table 4.

The estimates of the number of casualties $N$ increase as the amount of assumed positive dependence increases, i.e. as $\xi$ decreases, as expected. When $\xi = 0.9$, the posterior mean of 10155 and 95% credible
Figure 3: Posterior density of $N$ under each identifying assumption, using the LCM prior for $\tilde{\pi}$ of Manrique-Vallier (2016) and the negative-binomial prior for $N$.

Table 4: Posterior means and 95% credible intervals for $N$ under each identifying assumption, using the LCM prior for $\tilde{\pi}$ of Manrique-Vallier (2016) and the negative-binomial prior for $N$.

| $\xi$  | Posterior Mean | Credible Interval |
|--------|----------------|-------------------|
| 1      | 9359           | [7967, 11059]     |
| 0.9    | 10155          | [8607, 12038]     |
| 0.8    | 11147          | [9419, 13258]     |
| 0.7    | 12419          | [10451, 14816]    |

interval of [8607, 12038] are still largely compatible with the posterior mean and credible interval under independence. Thus our estimates under independence are not sensitive to this small amount of positive dependence. However, this is not still the case under stronger positive dependence. When $\xi = 0.7$, the 95% credible interval of [10451, 14816] barely overlaps with the credible interval under independence, and further it does not contain the posterior mean under independence. While this may seem like cause for concern, we note that these estimates under stronger positive dependence are still within an order of magnitude of the estimates under independence, and all credible intervals in this sensitivity analysis fall within the confidence interval of Spiegel and Salama (2000).
7 Discussion

In this article we revisited the framing of MSE as a missing data problem and proposed a Bayesian approach to MSE that places the identifying assumption front and center in the MSE workflow. A natural next step is to develop new explicit identifying assumptions, for situations where the identifying assumptions described in Section 4 can not be justified in the context of a given data set. We believe that this is an extremely under-researched problem that will hopefully gain attention with the re-framing of MSE we present in this article.

The presentation of MSE in this article was focused on estimating the size of a single population. When the population can be stratified based on observed covariates, such as location or time, it may be desirable to estimate the population sizes within each strata. In theory, the methodology developed in this article could be applied independently to each strata. However, stratification can lead to sparse contingency tables, which need significant regularization through the prior for \( \hat{\pi} \). In this case, it would be desirable to develop observed data models that borrow strength across strata.
A Appendix A: Conditional Identifiability in Models for Heterogeneity

The purpose of this appendix is to show how common models for heterogeneity fit into the model described in Section 2.2 and to provide results regarding conditional identifiability in a particular family of heterogeneous models. The material presented in Sections A.2, A.3, A.4, and A.5 previously appeared in an unpublished preprint written by the first author.¹

A.1 Models for Heterogeneity

Consider the following heterogeneous model

\[ \pi^i \sim Q, \quad x_i | \pi^i \sim \text{Categorical}(\pi^i), \]  

(A.1)

where \( \pi^i = \{ \pi_i^h \}_{h \in H} \in S^{2^K-1} \) for \( i = 1, \ldots, N \). Under this model each individual has its own set of cell probabilities, \( \pi^i \), drawn from some mixing distribution \( Q \) on \( S^{2^K-1} \). Working with the heterogeneous model in (A.1) is equivalent, after marginalizing out \( \pi^i \), to working with the complete-data distribution in (A), where \( \pi := \pi_Q = E_Q(\pi^i) \) and \( E_Q \) denotes the expectation with respect to the mixing distribution \( Q \). This is a consequence of the data only providing information about the first moment of the mixing distribution. Suppose \( Q \) is a family of mixing distributions on \( S^{2^K-1} \). For \( Q \in \mathcal{Q} \), let \( \pi_{Q,0} \) denote the induced unobserved cell probability and \( \tilde{\pi}_Q \) denote the induced observed cell probabilities. The parameter space induced by the family \( \mathcal{Q} \), as a subset of the observed-data parameterization, can then be written as \( \Omega_Q = \{ N, \pi_0, \tilde{\pi} | N \in \mathbb{N}, \pi_0 = \pi_{Q,0} \text{ and } \tilde{\pi} = \tilde{\pi}_Q \text{ for some } Q \in \mathcal{Q} \} \).

The general heterogeneous model in (A.1) captures common models for heterogeneity, including the \( M_h \) and \( M_{th} \) models (Otis et al., 1978). The \( M_{th} \) model assumes the individual cell probabilities take the form \( \pi_h^i = \prod_{k=1}^K (q_k^i)^{h_k} (1 - q_k^i)^{1-h_k} \), where \( (q_1^i, \ldots, q_K^i) \sim Q \) and \( Q \) is a mixing distribution on \( (0, 1)^K \). Under this model, conditional on an individual’s sampling probabilities, \( (q_1^i, \ldots, q_K^i) \), each individual is independently sampled by each list. The \( M_h \) model is a submodel of the \( M_{th} \) model that assumes that the

¹Aleshin-Guendel, S. (2020). On the Identifiability of Latent Class Models for Multiple-Systems Estimation. arXiv preprint arXiv:2008.09865
individual sampling probabilities, \((q_1^i, \ldots, q_K^i)\), are the same for each list, i.e. \(q_1^i = \cdots = q_K^i\). Thus the \(M_h\) model assumes individuals have the same probability of being sampled by each list. After marginalizing out \(\pi^i\), this enforces a symmetry where the probability of appearing in \(k\) lists is the same for each subset of \(k\) lists. We do not believe this is plausible in human population settings.

A.2 Conditional Identifiability in \(M_{th}\) Models

While there exists a literature characterizing identifiability in \(M_h\) models [Huggins 2001, Link 2003, Holzmann et al. 2006, Link 2006], no such results exist for \(M_{th}\) models. The purpose of this section is to provide a mechanism for verifying whether the \(M_{th}\) model \(P_{\Omega_Q}\) is conditionally identifiable based on moments of the mixing distributions \(Q \in \mathcal{Q}\), analogously to the results for \(M_h\) models presented in Holzmann et al. (2006).

Before proving the main theorem of this section, we have the following lemma, which tells us that for any mixing distribution \(Q\) on \((0, 1)^K\), the induced cell probabilities, \(\pi_Q\), only depend on \(Q\) through its mixed moments.

Lemma A.1. For any \(h \in H^*\), \(\pi_Q,h = \sum_{h' \in H^*} c_{h,h'} m_{Q,h'}\) where \(c_{h,h'} = \sum_{k=1}^K h'_k - h_k \prod_{k=1}^K I(h_k \leq h'_k)\) and \(m_{Q,h'} = \mathbb{E}_Q\left(\prod_{k=1}^K q_{h'_k}^{h_k}(1 - q_k)^{1-h_k}\right)\).

Proof. For all \(h \in H^*\), \(\prod_{k=1}^K q_k^{h_k}(1 - q_k)^{1-h_k} = \sum_{h' \in H^*} c_{h,h'} \prod_{k=1}^K q_k^{h'_k}\) by an application of the multinomial theorem (a generalization of the binomial theorem). The result follows from taking the expectation over both sides with respect to \(Q\).

We can restate Lemma A.1 in matrix form. Letting \(\pi_Q = (\pi_Q,h)_{h \in H^*}\) and \(m_Q = (m_Q,h)_{h \in H^*}\), we have that \(\pi_Q^* = C m_Q\), where \(C = (c_{h,h'})_{h \in H^*, h' \in H^*}\). \(C\) is invertible as it is upper triangular with non-zero diagonal entries. We are now ready to prove Theorem A.1.

Theorem A.1. For any two distributions \(Q, R\) on \((0, 1)^K\), \(\tilde{\pi}_Q = \tilde{\pi}_R\) is equivalent to \(m_Q = A m_R\) for some \(A > 0\).

Proof. \(\tilde{\pi}_Q = \tilde{\pi}_R\) is equivalent to \(\pi_Q^*/(1 - \pi_Q^0) = \pi_R^*/(1 - \pi_R^0)\). Rearranging terms we have that \(\pi_Q^* = \pi_R^*(1 - \pi_Q^0)/(1 - \pi_R^0)\), and thus \(\pi_Q^* = A \pi_R^*\), where \(A = (1 - \pi_Q^0)/(1 - \pi_R^0) > 0\). Using Lemma A.1 this is equivalent to \(C m_Q = A C m_R\), and thus \(m_Q = A m_R\) due to the invertibility of \(C\).
The immediate consequence of Theorem A.1 is that to verify conditional identifiability of an \(M_h\) model \(\mathcal{P}_{\Omega,Q}\), one can demonstrate that if \(m_Q = A m_R\) for some \(Q, R \in \mathcal{Q}\), then \(\pi_{Q,0} = \pi_{R,0}\). We use this mechanism in the next section to characterize when latent class models (LCMs) are conditionally identifiable.

### A.3 Conditional Identifiability of Latent Class Models

We denote the family of mixing distributions corresponding to LCMs with \(J\) classes by \(\mathcal{Q}_J = \{Q = \sum_{j=1}^{J} \nu_{Q,j} \prod_{k=1}^{K} \delta_{q_{Q,j,k}} \mid \nu_{Q,j} \geq 0, \sum_{j=1}^{J} \nu_{Q,j} = 1, q_{Q,jk} \in (0,1)^K\}\), so that \(P_{\Omega,\mathcal{Q}_J}\) is equivalent to \(P_{\Omega,LCM,J}\) from Section 3.2. To provide necessary and sufficient conditions for \(P_{\Omega,\mathcal{Q}_J}\) to be conditionally identifiable, we restrict the family of mixing distributions to \(\mathcal{Q}_J = \{Q = \sum_{j=1}^{J} \nu_{Q,j} \prod_{k=1}^{K} \delta_{q_{Q,j,k}} \mid \nu_{Q,j} \geq 0, \sum_{j=1}^{J} \nu_{Q,j} = 1, q_{Q,jk} \in (0,1)^K, q_{Q,jk} \neq q_{Q,j'k} \text{ for } j \neq j'\}\). This restriction makes the mild assumption that each class' sampling probabilities are distinct, which simplifies the proof of Theorem A.2. Loosening this restriction could only make the conditions on \(J\) for \(\mathcal{Q}_J\) to be identifiable stricter, and thus the conclusions we reach in Section A.6 would still stand for families where this restriction is violated.

There are \(J(K + 1) - 1\) parameters in \(\mathcal{Q}_J\), thus when \(P_{\Omega,\mathcal{Q}_J}\) is conditionally identifiable, \(J\) satisfies \(J(K + 1) - 1 \leq 2^K - 2\), as the observed cell probabilities, \(\tilde{\pi}_Q\), are \(2^K - 2\) dimensional. However, we now prove that \(J\) must satisfy a stricter condition for \(P_{\Omega,\mathcal{Q}_J}\) to be conditionally identifiable. In Section A.6 we discuss some limitations of this result.

**Theorem A.2.** \(P_{\Omega,\mathcal{Q}_J}\) is conditionally identifiable iff \(2J \leq K\).

**Proof.** We will first show that if \(2J \leq K\), then \(P_{\Omega,\mathcal{Q}_J}\) is conditionally identifiable. The proof of this direction is similar in spirit to the proofs of Theorem 2 in Holzmann et al. (2006) and Theorem 1 in Pezzotti et al. (2019), which were both concerned with characterizing the identifiability of the \(M_h\) analogue of \(P_{\Omega,\mathcal{Q}_J}\).

Assume \(2J \leq K\), and let \(Q, R \in \mathcal{Q}_J\) such that \(m_Q = A m_R\) for some \(A > 0\), so that we have the following system of equations:

\[
\sum_{j=1}^{J} \nu_{Q,j} \prod_{k=1}^{K} q_{Q,j,k} - A \sum_{j=1}^{J} \nu_{R,j} \prod_{k=1}^{K} q_{R,j,k} = 0 \quad (\mathbf{h} \in H^*). \tag{A.2}
\]

Let \(\mathcal{I}_Q = \{j \mid q_{Q,j} \notin (q_{R,1}, \ldots, q_{R,J})\}\) and \(\mathcal{I}_R = \{j \mid q_{R,j} \notin (q_{Q,1}, \ldots, q_{Q,J})\}\), where \(q_{Q,j} = (q_{Q,j1}, \ldots, q_{Q,jK})\)
and \( q_{R,j} = (q_{R,j1}, \ldots, q_{R,jK}) \). We can then rewrite (A.2) as

\[
\sum_{j=1}^{J} y_j \prod_{k=1}^{K} q_{Q,jk} - A \sum_{i \in I_R} \nu_{R,j} \prod_{k=1}^{K} q_{R,jk} = 0 \quad (h \in H^*),
\]

where \( y_j = \nu_{Q,j} \) if \( j \in I_Q \) and \( y_j = \nu_{Q,j} - A \nu_{R,j'} \) for some \( j' \in \{1, \ldots, J\} \setminus I_R \) otherwise. Letting \( m = |I_R| = |I_Q| \) and labelling the elements of \( I_R \) as \( i_1, \ldots, i_m \), the system of equations in (A.3) can be written in matrix form as \( \Lambda \mathbf{y} = \mathbf{0} \), where

\[
\Lambda = \begin{pmatrix}
q_{Q,1K} & \cdots & q_{Q,JK} & q_{R,1K} & \cdots & q_{R,i_mK} \\
\vdots & \ddots & \vdots & \ddots & \vdots & \vdots \\
\prod_{k=1}^{K} q_{Q,1k} & \cdots & \prod_{k=1}^{K} q_{Q,jk} & \prod_{k=1}^{K} q_{R,1k} & \cdots & \prod_{k=1}^{K} q_{R,i_mk} \\
\vdots & \ddots & \vdots & \ddots & \vdots & \vdots \\
\prod_{k=1}^{K} q_{Q,1k} & \cdots & q_{Q,jK} & \prod_{k=1}^{K} q_{R,1k} & \cdots & \prod_{k=1}^{K} q_{R,i_mk}
\end{pmatrix} \begin{pmatrix}
y_1 \\
\vdots \\
y_J \\
-A \nu_{R,i1} \\
\vdots \\
-A \nu_{R,i_m}
\end{pmatrix},
\]

and the rows of \( \Lambda \) are indexed by \( h \in H^* \). In Section A.4 we prove that \( \Lambda \) is full rank, and thus \( \mathbf{y} = \mathbf{0} \), for any \( m \in \{0, \ldots, J\} \). The proof of this direction concludes by examining three possible cases.

**Case 1.** Suppose \( m = 0 \), i.e. for each \( j \in \{1, \ldots, J\} \), there exists some \( j' \in \{1, \ldots, J\} \) such that \( q_{Q,j} = q_{R,j'} \) and \( \nu_{Q,j} = A \nu_{R,j'} \). As \( \sum_{j=1}^{J} \nu_{Q,j} = \sum_{j=1}^{J} \nu_{R,j} = 1 \), this implies that \( A = 1 \) and thus \( \pi_{Q,0} = \pi_{R,0} \).

**Case 2.** Suppose \( m \in \{1, \ldots, J - 1\} \), i.e. for each \( j \in \{1, \ldots, J\} \setminus I_Q \), there exists some \( j' \in \{1, \ldots, J\} \setminus I_R \) such that \( q_{Q,j} = q_{R,j'} \) and \( \nu_{Q,j} = A \nu_{R,j'} \). Further, for each \( j \in I_Q \) and \( j' \in I_R \nu_{Q,j} = \nu_{R,j'} = 0 \). We can thus ignore the classes \( j \in I_Q \) and \( j' \in I_R \). As \( \sum_{j=1}^{J} \nu_{Q,j} = \sum_{j=1}^{J} \nu_{R,j} = 1 \), this implies that \( A = 1 \) and thus \( \pi_{Q,0} = \pi_{R,0} \).

**Case 3.** Suppose \( m = J \), i.e. for each \( j \in \{1, \ldots, J\} \), there exists no \( j' \in \{1, \ldots, J\} \) such that \( q_{Q,j} = q_{R,j'} \). Then \( \nu_{Q,j} = \nu_{R,j} = 0 \) for \( j \in \{1, \ldots, J\} \), which is a contradiction.

We will now show that if \( 2J > K \), then \( \mathcal{P}_{\Omega_Q,j} \) is not conditionally identifiable. To do so we will provide explicit \( Q, R \in Q_J \) such that \( \pi_{Q,0} \neq \pi_{R,0} \), but \( m_Q = Am_R \) for \( A > 0 \). This counterexample is modified from Tahmasebi et al. (2018), who studied identifiability of families of LCMs outside of the multiple-systems estimation context where \( n_0 \) is observed. Choose \( J \) such that \( 2J > K \). For \( j \in \{1, \ldots, J\} \), let
\[ \nu_{Q,J} = \left(\frac{2^J}{2^J-1}\right) \] and \[ \nu_{R,J} = \left(\frac{2^J}{2^J-1}\right). \]

For \( j \in \{1, \ldots, J\} \) and \( k \in \{1, \ldots, K\} \), let \( q_{Q,jk} = \alpha(2^j) \) and \( q_{R,jk} = \alpha(2^j - 1) \) where \( 0 < \alpha < 1/(2J) \). We thus have that \( Q, R \in Q_J \), where clearly \( Q \neq R \).

In Section A.5 we prove that for these choices of \( Q, R \), \( m_Q = Am_R \) for \( A > 0 \) such that \( A \neq 1 \), and thus \( \pi_Q,0 \neq \pi_R,0 \).

\[ \square \]

A.4 Proof that \( \Lambda \) is Full Rank

We will prove that \( \Lambda \) is full rank for any \( m \in \{0, \ldots, J\} \) by proving a stronger result. Recall that \( K \geq 2 \) and let \( x_{\ell k} \in (0,1) \) for \( \ell \in \{1, \ldots, K\} \) and \( k \in \{1, \ldots, K\} \), such that \( x_{\ell k} \neq x_{\ell k'} \) for \( k \neq k' \). Let

\[
X^K = \begin{pmatrix}
    x_{1K} & \cdots & x_{KK} \\
    \vdots & \ddots & \vdots \\
    \Pi_{k=1}^K x_{1k} & \cdots & \Pi_{k=1}^K x_{Kk} \\
    \vdots & \ddots & \vdots \\
    \Pi_{k=1}^K x_{1k} & \cdots & \Pi_{k=1}^K x_{Kk}
\end{pmatrix},
\]

where the rows of \( X^K \) are indexed by \( h \in H^* \). We will show that \( X^K \) is full rank by induction on \( K \). This implies that \( \Lambda \) is full rank, as \( J + m \leq 2J \leq K \) by assumption for any \( m \in \{0, \ldots, J\} \).

For the base case when \( K = 2 \), verifying \( X^2 \) is full rank is straightforward. Assume that \( X^{K-1} \) is full rank. Let \( v \in \mathbb{R}^{K \times 1} \) be such that \( X^K v = 0 \). For each \( h' \in \{h' \in H^* \mid h'_K = 0\} \) we have that \( v_K \prod_{k=1}^{K-1} x_{Kk} = -\sum_{\ell=1}^{K-1} v_\ell \Pi_{k=1}^{K-1} x_{\ell k} \), which implies that \( \sum_{\ell=1}^{K-1} v_\ell (x_{\ell K} - x_{K K}) \prod_{k=1}^{K-1} x_{\ell k} = 0 \). For \( \ell \in \{1, \ldots, K-1\} \), let \( v'_\ell = v_\ell (x_{\ell K} - x_{K K}) \) and \( v' = (v'_1, \ldots, v'_{K-1}) \). This leads to the system of equations \( X^{K-1} v' = 0 \). By the inductive assumption, \( v' = 0 \). Since \( x_{\ell K} \neq x_{K K} \) for \( \ell \in \{1, \ldots, K-1\} \), we have that \( v_\ell = 0 \) for \( \ell \in \{1, \ldots, K-1\} \), and thus \( v_K = 0 \).

A.5 Proof of Counterexample

We will now prove that \( m_{Q,h} = Am_{R,h} \) for all \( h \in H^* \), where \( A = (2^{2J-1})/(2^{2J-1} - 1) \neq 1 \). Define the function \( h(x) = (1 - e^{\alpha x})^{2J} = \sum_{i=0}^{2J} \left(\frac{2^J}{i!}\right)(-1)^i e^{\alpha ix} \). For \( t \in \{1, \ldots, K\} \), we can differentiate the series representation of \( h \) to find that \( h^{(t)}(x) = \sum_{i=0}^{2J} \left(\frac{2^J}{i!}\right)(-1)^i e^{\alpha ix} \) and thus \( h^{(t)}(x)|_{x=0} = \sum_{i=0}^{2J} \left(\frac{2^J}{i!}\right)(-1)^i = \sum_{i=1}^{2J} \left(\frac{2^J}{i!}\right)(-1)^i(\alpha)^i \). We can alternatively differentiate the non-series representation of \( h \) using the fact that
\( t \leq K < 2J \) and the chain rule for higher order derivatives to find that \( h^{(t)}(x)|_{x=0} = 0 \). Let \( h \in \mathcal{H}^{*} \) and \( t = \sum_{k=1}^{K} h_{k} \in \{1, \ldots, K\} \). The desired result follows as

\[
m_{Q,h} - Am_{R,h} = \sum_{j=1}^{J} \nu_{Q,j} \prod_{k=1}^{K} q_{Q,k}^{h_{k}} - A \sum_{j=1}^{J} \nu_{R,j} \prod_{k=1}^{K} q_{R,k}^{h_{k}}
\]

\[
= \sum_{j=1}^{J} \binom{2J}{2j} (2^{2J-1} - 1)^{-1} \prod_{k=1}^{K} (\alpha(2j))^{h_{k}} - A \sum_{j=1}^{J} \binom{2J}{2j-1} (2^{2J-1} - 1)^{-1} \prod_{k=1}^{K} (\alpha(2j-1))^{h_{k}}
\]

\[
= (2^{2J-1} - 1)^{-1} \sum_{i=1}^{2J} (-1)^i (\alpha)^i = (2^{2J-1} - 1)^{-1} \{ h^{(t)}(x)|_{x=0} \} = 0.
\]

A.6 Limitations of Theorem A.2

Theorem A.2 shows that \( \mathcal{P}_{\Omega_{Q,J}} \) is not conditionally identifiable if \( 2J > K \) by counterexample, by demonstrating two mixing distributions \( Q, R \in \mathcal{Q}_{J} \) where \( \tilde{\pi}_{Q} = \tilde{\pi}_{R} \) but \( \pi_{Q,0} \neq \pi_{R,0} \). Within each latent class of \( Q \) and \( R \), the sampling probabilities were the same, meaning \( Q \) and \( R \) can be seen as mixing distributions of an \( M_{h} \) model. It would be interesting in future work to see whether further restrictions on \( \Omega_{Q,J} \), for example restrictions not allowing the sampling probabilities within latent classes to be equal, lead to different results concerning conditional identifiability. Another interesting route would be to see whether results concerning generic identifiability of latent class models \cite{Allman2009} could be applied to the multiple-systems estimation setting.

However, this does not mean Theorem A.2 is not a practically useful result. Theorem A.2 provides assumptions under which we have formal statistical guarantees for when we can estimate the parameters in \( \mathcal{P}_{\Omega_{Q,J}} \): the parameters of \( \mathcal{P}_{\Omega_{Q,J}} \) can be consistently estimated if \( 2J \leq K \). When \( 2J > K \) we currently have no such guarantees. In Appendix C we demonstrate this reality across a variety of simulation studies.

B Appendix B: Identifying Assumption Derivations

The purpose of this appendix is to derive the identifying assumptions associated with no-highest-order interaction assumption and the \( K' \)-list marginal no-highest-order interaction assumption.
B.1 Derivation for No-Highest-Order Interaction Assumption

Recall from Section 3.1 that we have the following relationship between the cell probabilities and the highest order interaction, \( \lambda_1: \prod_{h \in H} \pi_h^{I_{\text{odd}}(h)}/\prod_{h \in H} \pi_h^{I_{\text{even}}(h)} = \exp\{(1 - I_{\text{even}}(\lambda_1))\}\), where \( I_{\text{odd}}(h) = I(\sum_{k=1}^{K}(2 - h_k) \text{ is odd})\) and \( I_{\text{even}}(h) = I(\sum_{k=1}^{K}2 - h_k)\). Suppose we fix \( \lambda_1 \in \mathbb{R}\), or equivalently \( \xi = \exp\{(1 - I_{\text{even}}(\lambda_1))\} \in \mathbb{R}^+\). Under this assumption we have that \( \prod_{h \in H} \pi_h^{I_{\text{odd}}(h)}/\prod_{h \in H} \pi_h^{I_{\text{even}}(h)} = \xi\).

Multiplying the left-hand side by \( 1 = \left(\frac{1 - \pi_0}{1 - \pi_0}\right)^{2^{K-1}}\), we find that \( \tilde{\Pi}_{\text{odd}}/\{[\pi_0/(1 - \pi_0)]\tilde{\Pi}_{\text{even}}\} = \xi\), where \( \tilde{\Pi}_{\text{odd}} = \prod_{h \in H^*} \tilde{\pi}_h^{I_{\text{odd}}(h)}\) and \( \tilde{\Pi}_{\text{even}} = \prod_{h \in H^*} \tilde{\pi}_h^{I_{\text{even}}(h)}\). Rearranging terms and solving for \( \pi_0\), we find that the assumption that \( \xi \) is a fixed value corresponds to the explicit functional relationship

\[
T(\tilde{\pi}) = \frac{\tilde{\Pi}_{\text{odd}}/\tilde{\Pi}_{\text{even}}}{\xi + \tilde{\Pi}_{\text{odd}}/\tilde{\Pi}_{\text{even}}}.
\]

The identifying assumption corresponding to the no-highest-order interaction assumption is recovered by setting \( \lambda_1 = 0\), or equivalently \( \xi = 1\): \( T(\tilde{\pi}) = (\tilde{\Pi}_{\text{odd}}/\tilde{\Pi}_{\text{even}})/(1 + \tilde{\Pi}_{\text{odd}}/\tilde{\Pi}_{\text{even}})\). The observed-data distribution is not restricted by the assumption that the highest-order interaction is fixed, and thus models that use this assumption without any extra assumptions regarding the observed cell probabilities are nonparametric identified.

B.2 Derivation for \( K'\)-list Marginal No-Highest-Order Interaction Assumption

Suppose we assume that \( \prod_{g \in G} \pi_g^{I_{\text{odd}}(g)}/\prod_{g \in G} \pi_g^{I_{\text{even}}(g)} = \xi\), where \( \xi \in \mathbb{R}^+\) is fixed. Multiplying the left-hand side by \( 1 = \left(\frac{1 - \pi_0}{1 - \pi_0}\right)^{2^{K'-1}}\), we find that \( \tilde{\Pi}_{\text{odd},+}/\{[\pi_0/(1 - \pi_0)] + \tilde{\pi}_{0,+}\tilde{\Pi}_{\text{even},+}\} = \xi\), where \( \tilde{\Pi}_{\text{odd},+} = \prod_{g \in G^*} \tilde{\pi}_g^{I_{\text{odd}}(g)}\) and \( \tilde{\Pi}_{\text{even},+} = \prod_{g \in G^*} \tilde{\pi}_g^{I_{\text{even}}(g)}\). Rearranging terms and solving for \( \pi_0\), we find that the assumption that \( \xi \) is a fixed value corresponds to the explicit functional relationship

\[
T(\tilde{\pi}) = \frac{\tilde{\Pi}_{\text{odd},+}/\tilde{\Pi}_{\text{even},+} - \xi \tilde{\pi}_{0,+}}{\xi + (\tilde{\Pi}_{\text{odd},+}/\tilde{\Pi}_{\text{even},+}) - \xi \tilde{\pi}_{0,+}}.
\]

The identifying assumption corresponding to the \( K'\)-list marginal no-highest-order interaction assumption is recovered by setting \( \xi = 1\): \( T(\tilde{\pi}) = (\tilde{\Pi}_{\text{odd},+}/\tilde{\Pi}_{\text{even},+} - \tilde{\pi}_{0,+})/(1 + \tilde{\Pi}_{\text{odd},+}/\tilde{\Pi}_{\text{even},+} - \tilde{\pi}_{0,+})\).

As noted in Section 4.3, the \( K'\)-list marginal no-highest-order interaction assumption does not imply that there is no highest-order interaction for all \( K \) lists, as \( \prod_{h \in H} \pi_h^{I_{\text{odd}}(h)}/\prod_{h \in H} \pi_h^{I_{\text{even}}(h)} = (\tilde{\Pi}_{\text{odd}}/\tilde{\Pi}_{\text{even}}) \times (\tilde{\Pi}_{\text{odd},+}/\tilde{\Pi}_{\text{even},+} - \tilde{\pi}_{0,+}) \neq 1 \) in general.
Appendix C: Latent Class Model Simulations

The purpose of this appendix is to conduct simulation studies demonstrating the practical implications of Theorem A.2. In particular, we present a variety of simulations exploring the frequentist properties of the Bayesian LCM of Manrique-Vallier (2016). In each example we generate 200 data sets from the model in (A.1) for a given number of lists $K$ and a fixed parameter setting of $\theta \in \Omega_J$, i.e. a fixed population size $N$ and a $J$-class LCM $Q \in \mathcal{Q}_J$. For all examples we will use $N \in \{2000, 10000, 100000\}$. For each simulated data set, we fit the Bayesian LCM of Manrique-Vallier (2016) as implemented in the R package LCMCR, using $J$ latent classes (i.e. the same number that generated the data) and the default prior for $\nu$, by running the Gibbs sampler implemented in LCMCR for 250,000 iterations, with the first 50,000 tossed for burn-in. We note that LCMCR uses the improper scale prior for $N$, i.e. $p(N) \propto 1/N$, and a flat prior for $q_i$, i.e. $q_{jk} \overset{i.i.d.}{\sim} \text{Unif}(0,1)$, which cannot be changed. For each parameter setting of $\theta \in \Omega_J$, we examine the frequentist performance of the posterior median, 95% credible interval, and 50% credible interval for estimating the unobserved cell probability, $\pi_0$, through the sample mean of the posterior medians, the sample coverage of the 95% credible intervals, the sample mean of the 95% credible interval widths over the 200 replications, the sample coverage of the 50% credible intervals, and the sample mean of the 50% credible interval widths over the 200 replications.

C.1 Example 1

In this example we consider data from $K = 2$ lists generated from the two-class LCM $Q_{1a}$ with parameters given in Table 5. Under $Q_{1a}$, $\hat{\pi}_{Q_{1a},(0,1)} = 0.276$, $\hat{\pi}_{Q_{1a},(1,0)} = 0.276$, $\hat{\pi}_{Q_{1a},(1,1)} = 0.448$, and $\pi_{Q_{1a},0} = 0.316$. There exists another two-class LCM $Q_{1b}$, with parameters given in Table 5 such that $\hat{\pi}_{Q_{1a}} = \hat{\pi}_{Q_{1b}}$ but $\pi_{Q_{1b},0} = 0.219$. Because $\mathcal{P}_{\Omega_Q}$ is not conditionally identified when $K = 2$, if we try to perform estimation within $\mathcal{P}_{\Omega_Q}$, which contains the true data generating model, there is no guarantee that we can estimate well the cell probabilities and population size which generated the data. This example was constructed using the counterexample used to prove Theorem A.2.

The results of the simulation using data generated using the LCM $Q_{1a}$ are presented in Table 6. We see that the posterior median has a negative bias that does not vanish as $N$ increases. One may have
Table 5: Parameters of two latent class models, $Q_{1a}$ and $Q_{1b}$ (rounded for presentation)

|     | $\nu_1$ | $\nu_2$ | $q_{11}$ | $q_{12}$ | $q_{21}$ | $q_{22}$ |
|-----|---------|---------|---------|---------|---------|---------|
| $Q_{1a}$ | 0.500  | 0.500  | 0.248  | 0.248  | 0.743  | 0.743  |
| $Q_{1b}$ | 0.857  | 0.143  | 0.495  | 0.495  | 0.990  | 0.990  |

thought that the posterior median might possibly be a good estimator for $\pi_{Q_{1b},0} = 0.219$ since $Q_{1a}$ and $Q_{1b}$ induce the same observed-data distribution. However, the posterior median is also negatively biased for estimating $\pi_{Q_{1b},0}$, which suggests there are other LCMs in $Q_2$ that induce very similar observed-data distributions to $Q_{1a}$ and $Q_{1b}$ but with different induced unobserved cell probabilities. While the 95% credible interval has nominal coverage when $N = 2000$, as $N$ increases, coverage decreases and is no longer nominal. The 50% credible interval have essentially 0 coverage for settings of $N$, even for $N = 2000$ where the 95% credible interval has nominal coverage. This suggests the 95% credible interval only has nominal coverage at $N = 2000$ due to wide tails of the posterior for $N$.

Table 6: Results of the simulation study where data was generated from the two-class latent class model $Q_{1a}$. Truth is $\pi_{Q_{1a},0} = 0.316$.

| $N$   | Mean | Posterior Median | 95% CI Coverage | Mean | 95% CI Width | 50% CI Coverage | Mean | 50% CI Width |
|-------|------|------------------|-----------------|------|--------------|-----------------|------|--------------|
| 2000  | 0.148| 0.955            | 0.332           | 0.000| 0.029        |
| 10000 | 0.146| 0.730            | 0.316           | 0.000| 0.023        |
| 100000| 0.151| 0.265            | 0.167           | 0.055| 0.037        |

C.2 Example 2

One may object to the practicality of Example 1, as it examined a two class LCM constructed using the counterexample from the proof of Theorem A.2, and is thus an $M_h$ LCM. So we now consider the following example. Manrique-Vallier (2016) presented a simulation study with $K = 5$ lists where data was generated from a LCM with $J = 2$ classes, which we reproduce in Table 7 The parameters of this LCM were based on a hypothetical population where a small proportion of people have a high probability of being observed, and a large proportion of people have a small probability of being observed, which is plausible in some human
rights applications.

Table 7: Parameters of latent class model which generated data in simulation of [Manrique-Vallier](#) (2016).

| Class | Sampling probabilities, $q$ |
|-------|-----------------------------|
|       | List 1 | List 2 | List 3 | List 4 | List 5 |
| 1     | 0.900  | 0.033  | 0.033  | 0.099  | 0.132  | 0.033  |
| 2     | 0.100  | 0.660  | 0.825  | 0.759  | 0.990  | 0.693  |

Suppose we only observed lists three and four, so that we have data from $K = 2$ lists generated from the two-class LCM $Q_2$ with parameters given in Table 8. Under $Q_2$, $\pi_{Q_2,0} = 0.704$. Just as in the previous example, because $P_{\Omega_{Q_2}}$ is not conditionally identified when $K = 2$, if we try to perform estimation within $P_{\Omega_{Q_2}}$, which contains the true data generating model, there is no guarantee that we can estimate well the cell probabilities and population size which generated the data. The results of the simulation using data generated using the LCM $Q_2$ are presented in Table 9. We see that the posterior median has a large negative bias that does not vanish as $N$ increases, while the mean 95% and 50% credible interval widths decrease as $N$ increases. Further, the 95% and 50% credible intervals have essentially 0 coverage across all $N$.

Table 8: Parameters of latent class model $Q_2$

| $\nu_1$ | $\nu_2$ | $q_{11}$ | $q_{12}$ | $q_{21}$ | $q_{22}$ |
|---------|---------|----------|----------|----------|----------|
| 0.900   | 0.100   | 0.099    | 0.132    | 0.759    | 0.990    |

Table 9: Results of the simulation study where data was generated from the two-class latent class model $Q_2$.

Truth is $\pi_{Q_2,0} = 0.704$.

| $N$  | Mean Posterior Median | 95% CI Coverage | Mean 95% CI Width | 50% CI Coverage | Mean 50% CI Width |
|------|-----------------------|------------------|-------------------|-----------------|------------------|
| 2000 | 0.285                 | 0.000            | 0.408             | 0.000           | 0.055            |
| 10000| 0.283                 | 0.010            | 0.401             | 0.000           | 0.036            |
| 100000| 0.285                | 0.030            | 0.256             | 0.000           | 0.035            |
C.3 Example 3

In this example we present two more frequentist simulation studies based on only observing a subset of the five lists from the simulation of Manrique-Vallier (2016).

First suppose that we only observe lists two, three, and four from the simulation of Manrique-Vallier (2016), so that we have data from \( K = 3 \) lists generated from the two-class LCM \( Q_{3a} \) with parameters given in Table 10. Under \( Q_{3a} \), \( \pi_{Q_{3a},0} = 0.681 \). Because \( P_{\Omega_{Q_2}} \) is not conditionally identified when \( K = 3 \), if we try to perform estimation within \( P_{\Omega_{Q_2}} \), which contains the true data generating model, there is no guarantee that we can estimate well the cell probabilities and population size which generated the data. The results of the simulation using data generated using the LCM \( Q_{3a} \) are presented in Table 11. We see that the posterior median has a slight negative bias that becomes negligible as \( N \) increases. The 95\% credible intervals have over-coverage across the different settings of \( N \). The 50\% credible intervals have nominal coverage when \( N = 2000 \), but have over-coverage as \( N \) increases.

Table 10: Parameters of latent class model \( Q_{3a} \)

| Class | \( \nu \) | List 2 | List 3 | List 4 |
|-------|--------|-------|-------|-------|
| 1     | 0.900  | 0.033 | 0.099 | 0.132 |
| 2     | 0.100  | 0.825 | 0.759 | 0.990 |

Table 11: Results of the simulation study where data was generated from the two-class latent class model \( Q_{3a} \). Truth is \( \pi_{Q_{3a},0} = 0.681 \).

| \( N \) | Mean Posterior Median | 95\% CI Coverage | Mean 95\% CI Width | 50\% CI Coverage | Mean 50\% CI Width |
|---------|-----------------------|-------------------|--------------------|------------------|-------------------|
| 2000    | 0.622                 | 1.000             | 0.339              | 0.510            | 0.120             |
| 10000   | 0.667                 | 1.000             | 0.274              | 0.800            | 0.091             |
| 100000  | 0.682                 | 1.000             | 0.209              | 0.965            | 0.074             |

Suppose now we only observe lists two, three, four, and five from the simulation of Manrique-Vallier (2016), so that we have data from \( K = 4 \) lists generated from the two-class LCM \( Q_{3b} \) with parameters given...
in Table 12. Under $Q_{3b}$, $\pi_{Q_{3b}, 0} = 0.658$. Because $P_{\Omega_{Q_{3a}}}$ is conditionally identified when $K = 4$, we know that, since $P_{\Omega_{Q_{3a}}}$ contains the true data generating model, we can consistently estimate the cell probabilities and population size which generated the data. The results of the simulation using data generated using the LCM $Q_{3a}$ are presented in Table 13. We see that the posterior median has a negative bias that becomes negligible as $N$ increases, as expected. The 95% and 50% credible intervals have slight under-coverage when $N = 2000$, which becomes nominal as $N$ increases.

Table 12: Parameters of latent class model $Q_{3b}$

| Class | $\nu$ | List 2 | List 3 | List 4 | List 5 |
|-------|-------|--------|--------|--------|--------|
| 1     | 0.900 | 0.033  | 0.099  | 0.132  | 0.033  |
| 2     | 0.100 | 0.825  | 0.759  | 0.990  | 0.693  |

Table 13: Results of the simulation study where data was generated from the two-class latent class model $Q_{3b}$. Truth is $\pi_{Q_{3b}, 0} = 0.658$.

| $N$   | Mean Posterior Median | 95% CI Coverage | Mean 95% CI Width | 50% CI Coverage | Mean 50% CI Width |
|-------|-----------------------|-----------------|-------------------|-----------------|-------------------|
| 2000  | 0.631                 | 0.915           | 0.190             | 0.445           | 0.065             |
| 10000 | 0.653                 | 0.940           | 0.089             | 0.505           | 0.031             |
| 100000| 0.658                 | 0.955           | 0.028             | 0.485           | 0.010             |

C.4 Example 4

In this example we present three more frequentist simulation studies based on adding a third class to the LCM from the simulation study of Manrique-Vallier (2016), representing a small proportion of the population having a probability of being observed somewhere between the other two classes. The parameters of this new LCM are given in Table 14.

First suppose that we only observe lists two, three, and four from the LCM in Table 14, so that we have data from $K = 3$ lists generated from the three-class LCM $Q_{4a}$ with parameters given in Table 15. Under $Q_{4a}$,
Table 14: Parameters of latent class model which generated data in simulation of [Manrique-Vallier (2016)], with a third class added.

| Class | \( \nu \) | List 1 | List 2 | List 3 | List 4 | List 5 |
|-------|-----|-------|-------|-------|-------|-------|
| 1     | 0.700 | 0.033 | 0.033 | 0.099 | 0.132 | 0.033 |
| 2     | 0.200 | 0.275 | 0.250 | 0.200 | 0.300 | 0.325 |
| 3     | 0.100 | 0.660 | 0.825 | 0.759 | 0.990 | 0.693 |

\( \pi_{Q_{4a},0} = 0.613 \). Because \( P_{\Omega_{Q_{3}}} \) is not conditionally identified when \( K = 3 \), if we try to perform estimation within \( P_{\Omega_{Q_{3}}} \), which contains the true data generating model, there is no guarantee that we can estimate well the cell probabilities and population size which generated the data. The results of the simulation using data generated using the LCM \( Q_{4a} \) are presented in Table 16. We see that the posterior median has a negative bias that does not vanish as \( N \) increases. The 95\% credible intervals have over-coverage across the different settings of \( N \), while the 50\% credible intervals have under-coverage across the different settings of \( N \). Similar to Example 1 in Section C.1, this suggests the 95\% credible interval only has over-coverage due to wide tails of the posterior for \( N \).

Table 15: Parameters of latent class model \( Q_{4a} \)

| Class | \( \nu \) | List 1 | List 2 | List 3 |
|-------|-----|-------|-------|-------|
| 1     | 0.700 | 0.033 | 0.099 | 0.132 |
| 2     | 0.200 | 0.250 | 0.200 | 0.300 |
| 3     | 0.100 | 0.825 | 0.759 | 0.990 |

Next suppose that we only observe lists two, three, four, and five from the LCM in Table 14, so that we have data from \( K = 4 \) lists generated from the three-class LCM \( Q_{4b} \) with parameters given in Table 13. Under \( Q_{4b} \), \( \pi_{Q_{4b},0} = 0.569 \). Because \( P_{\Omega_{Q_{3}}} \) is not conditionally identified when \( K = 4 \), if we try to
Table 16: Results of the simulation study where data was generated from the two-class latent class model $Q_{4a}$. Truth is $\pi_{Q_{4a},0} = 0.613$.

| N   | Mean Posterior Median | 95% CI Coverage | Mean 50% CI Width | Mean 50% CI Coverage | Mean 50% CI Width |
|-----|-----------------------|-----------------|-------------------|----------------------|-------------------|
| 2000| 0.524                 | 1.000           | 0.387             | 0.210                | 0.119             |
| 10000| 0.537                | 1.000           | 0.364             | 0.150                | 0.102             |
| 100000| 0.538              | 1.000           | 0.323             | 0.175                | 0.096             |

Perform estimation within $\mathcal{P}_{\Omega_{Q_3}}$, which contains the true data generating model, there is no guarantee that we can estimate well the cell probabilities and population size which generated the data. The results of the simulation using data generated using the LCM $Q_{4b}$ are presented in Table 18. We see that the posterior median has a negative bias that decreases as $N$ increases. While the 95% and 50% credible intervals do not have nominal coverage, coverage improves as $N$ increases (but is still far from nominal even when $N = 100000$).

Table 17: Parameters of latent class model $Q_{4b}$

| Class | $\nu$ | List 1 | List 2 | List 3 | List 4 |
|-------|-------|--------|--------|--------|--------|
| 1     | 0.700 | 0.033  | 0.099  | 0.132  | 0.033  |
| 2     | 0.200 | 0.250  | 0.200  | 0.300  | 0.325  |
| 3     | 0.100 | 0.825  | 0.759  | 0.990  | 0.693  |

Table 18: Results of the simulation study where data was generated from the two-class latent class model $Q_{4b}$. Truth is $\pi_{Q_{4b},0} = 0.569$.

| N   | Mean Posterior Median | 95% CI Coverage | Mean 95% CI Width | Mean 50% CI Coverage | Mean 50% CI Width |
|-----|-----------------------|-----------------|-------------------|----------------------|-------------------|
| 2000| 0.469                 | 0.525           | 0.199             | 0.090                | 0.065             |
| 10000| 0.509                | 0.630           | 0.128             | 0.120                | 0.041             |
| 100000| 0.519               | 0.695           | 0.066             | 0.290                | 0.023             |
Next suppose that we observe all five lists from the LCM in Table 14 so that we have data from $K = 5$ lists generated from the three-class LCM which we will refer to as $Q_{4c}$. Under $Q_{4c}$, $\pi_{Q_{4c},0} = 0.536$. Because $\mathcal{P}_{\Omega_{Q_3}}$ is not conditionally identified when $K = 5$, if we try to perform estimation within $\mathcal{P}_{\Omega_{Q_3}}$, which contains the true data generating model, there is no guarantee that we can estimate well the cell probabilities and population size which generated the data. The results of the simulation using data generated using the LCM $Q_{4c}$ are presented in Table 19. We see that the posterior median has a negative bias that decreases as $N$ increases. While the 95% and 50% credible intervals do not have nominal coverage, coverage improves as $N$ increases.

Table 19: Results of the simulation study where data was generated from the two-class latent class model $Q_{4c}$. Truth is $\pi_{Q_{4c},0} = 0.536$.

| $N$  | Mean Posterior Median | 95% CI Coverage | Mean 95% CI Width | 50% CI Coverage | Mean 50% CI Width |
|------|-----------------------|-----------------|-------------------|-----------------|------------------|
| 2000 | 0.435                 | 0.415           | 0.169             | 0.050           | 0.055            |
| 10000| 0.500                 | 0.875           | 0.132             | 0.370           | 0.044            |
| 100000| 0.523               | 0.895           | 0.053             | 0.490           | 0.018            |

C.5 Takeaways

When using the model $\mathcal{P}_{\Omega_{Q_J}}$ for multiple-systems estimation, one is relying on the assumption that the data was generated from a distribution in $\mathcal{P}_{\Omega_{Q_J}}$. If a practitioner is comfortable with the assumption that $2J \leq K$, then we know the model is conditionally identified, and thus this assumption is a combination of an explicit identifying assumption (which is currently unknown) and possibly some restrictions on the observed-data distribution. Due to conditional identification, the practitioners have guarantees under this assumption that they can estimate the population size, and other parameters, well if their observed sample size $n$ is large enough. However, if a practitioner is not comfortable with this assumption, and chooses to use $J > K/2$, they have no such guarantees as they are using a model that is not conditionally identified.

Through the four example simulation studies in this appendix we saw examples where models that were not conditionally identified had good frequentist performance ($Q_{3a}$, $Q_{4a}$) and bad frequentist performance.
\((Q_1, Q_2, Q_{4b}, Q_{4c})\) according to some of our simulation summary measures. The good and bad frequentist performances could have been due to

- where the prior of Manrique-Vallier (2016) places mass in the parameter space \(\Omega_{Q_j}\) (e.g. good frequentist performance if it places enough prior mass around the true data generating parameters),

- whether there actually exists other LCMs in \(Q_j\) that induce similar observed cell probabilities to the true data generating parameters but a different unobserved cell probability (e.g. good frequentist performance if other LCMs do not exist with these properties),

- or some combination of the two previous factors.

We currently have no way to tease apart these factors and tell when a model that is not conditionally identified will have good or bad performance. This is a problem for using these models in practice, as we have no way to tell practitioners “under these assumptions the model will perform well”.

We believe there are two routes forward to combat this problem, if one wants to use LCMs for multiple-systems estimation. The first option is to further study technical results for conditional identification in LCMs. For example, as we discussed in Section A.6 suppose we can prove under further (practically relevant) restrictions on \(Q_j\) that \(P_{\Omega_{Q_j}}\) is conditionally identified for some \(J > K/2\). We would then be able to expand the range of models we could fit under which we had guarantees that we could estimate well the parameters of the model.

The other option is to study LCMs through the framework of partial identification (Tamer, 2010; Gustafson, 2010), which was recently used in multiple-systems estimation by Sun et al. (2020) for frequentist inference for partially-identified log-linear models. This would require both: 1) a better technical understanding of what parameters, or functions of parameters, of LCMs are not identified, and 2) placing substantively meaningful priors on the non-identified parameters (i.e. priors informed by substantive knowledge concerning the population of interest and how the data was collected) if a Bayesian approach is taken. Without 1), the best we can do in a Bayesian approach is to place substantively meaningful priors on all LCM parameters, i.e. on \(\Omega_{Q_j}\). The prior for \(\Omega_{Q_j}\) of Manrique-Vallier (2016) is based on the Dirichlet Process prior specification of Dunson and Xing (2009), which is a prior of technical convenience. Specifying
a substantively meaningful prior for $\Omega \Theta_j$ would require being able to specify a prior for the class membership probabilities $\nu$ and for the class specific observation probabilities $q$. It is difficult to imagine a scenario in which a practitioner would have knowledge of the population of interest and how the data was collected that could be incorporated into priors for all $J(K + 1) - 1$ of the parameters ($\nu$ and $q$).

While we do not believe that latent class models cannot be used for multiple-systems estimation (see our application in Section 6 where we use the LCM prior of Manrique-Vallier (2016) to induce a prior for the observed cell probabilities $\tilde{\pi}$), we do believe that there needs to be further research to understand under what assumptions LCMs do and do not perform well in practice. We discuss one further area of research before concluding this section. The start of this section began by assuming that a practitioner assumed their data was generated by a distribution in $P_{\Omega \Theta_j}$. It is not clear to the authors how in practice one would choose a specific value of $J$. In practice, how would a practitioner choose between $P_{\Omega \Theta_j}$ and $P_{\Omega \Theta_{j'}}$ for $J \neq J'$? What characteristics of the population being studied and the data collection process would allow one to differentiate between these two models? Research into understanding how to elicit plausible values of $J$ would help to justify the use of the model $P_{\Omega \Theta_j}$ in practice.

D Appendix D: Kosovo Analysis Using No-Highest-Order Interaction Assumption

The purpose of this appendix is to repeat the analysis of the Kosovo data set from Section 6 using the no-highest-order interaction assumption. We first discuss the implications of this identifying assumption in the context of the Kosovo data set before performing the analysis.

D.1 The No-Highest-Order Interaction Assumption

The Kosovo data set has $K = 4$ lists, which we will order (without loss of generality) so that the American Bar Association Central and East European Law Initiative (ABA) list is first, the Human Rights Watch (HRW) list is second, the Organization for Security and Cooperation in Europe (OSCE) list is third, and the list constructed from exhumation reports conducted on behalf of the International Criminal Tribunal for
the Former Yugoslavia (EXH) is fourth. Let $\text{Odds}(h_1 = 1 \mid h_2 = 1, h_3, h_4) = \frac{\pi_{(1,1,h_3,h_4)}}{\pi_{(0,1,h_3,h_4)}}$ denote the odds that an individual is observed in list 1, conditional on being observed in list 2 and the inclusion patterns $h_3, h_4$ for lists 3 and 4. For example, if $h_3 = 0$ and $h_4 = 1$, $\text{Odds}(h_1 = 1 \mid h_2 = 1, h_3 = 0, h_4 = 1)$ is the odds that an individual is observed in list 1, conditional on being observed in lists 2 and 4 and not being observed in list 3. Similarly let $\text{Odds}(h_1 = 1 \mid h_2 = 0, h_3, h_4) = \frac{\pi_{(1,0,h_3,h_4)}}{\pi_{(0,0,h_3,h_4)}}$ denote the odds that an individual is observed in list 1, conditional on not being observed in list 2 and the inclusion patterns $h_3, h_4$ for lists 3 and 4. We can then define $\text{OR}(h_3, h_4) = \frac{\text{Odds}(h_1 = 1 \mid h_2 = 1, h_3, h_4)}{\text{Odds}(h_1 = 1 \mid h_2 = 0, h_3, h_4)}$ as the odds ratio for lists 1 and 2, conditional on the inclusion patterns $h_3, h_4$ for lists 3 and 4. Following Section 4.1 the no-highest-order interaction assumption assumes that $\text{OR}(1,0)/\text{OR}(0,0) = \text{OR}(1,1)/\text{OR}(0,1)$, i.e. the highest-order interaction for the first three lists, conditional on not being observed in list 4, $\text{OR}(1,0)/\text{OR}(0,0)$, is equal to the highest-order interaction for the first three lists, conditional on being observed in list 4, $\text{OR}(1,1)/\text{OR}(0,1)$.

This assumption is obscure and hard to justify based on our knowledge of how the four lists were generated. As the validity of our analysis rests on this assumption being correct, we stress that we are not confident that this assumption holds, and thus we are not confident in the validity of the following analysis. These analyses should be viewed as a demonstration of the computational approach described in Section 5.2.

### D.2 Main Analysis

For each combination of prior for $N$ and $\tilde{\pi}$ described in Sections 6.2 and 6.3, we fit the corresponding model using the computational approach described in Section 5.2 using the no-highest-order interaction assumption. In particular, we emphasize that for each prior for $\tilde{\pi}$, we only drew samples from the corresponding $p_C(\tilde{\pi} \mid n)$ once. The posterior density for $N$ under each prior combination is displayed in Figure 4. Posterior means and 95% credible intervals for $N$ under each prior combination are displayed in Table 20. Assuming that there is no-highest-order interaction, under the negative-binomial prior for $N$ and LCM prior for $\tilde{\pi}$ of Manrique-Vallier (2016), we estimate there were 14071 civilian casualties, with a 95% credible interval of [9321, 21604]. This credible interval includes the point estimate from Spiegel and Salama (2000), but not from Iacopino et al. (2001).
When using the LCM prior for $\hat{\pi}$, the posterior distribution for $N$ is somewhat sensitive to our choice of prior for $N$, as under the “noninformative” improper scale prior for $N$ the posterior mean increases from 14071 to 14695, and the upper limit of the credible interval increases from 21604 to 23675. When considering the other priors for $\hat{\pi}$, the posterior distribution for $N$ is again somewhat sensitive to our choice of prior for $N$, where the posterior mean and credible interval limits are larger under the improper scale prior compared to the negative-binomial prior. Across the different priors for $\hat{\pi}$, the posteriors corresponding to the Dirichlet prior, the log-linear model prior, and the LCM prior of [Manrique-Vallier 2016] are in relative agreement. The posterior corresponding to the Dirichlet prior is the most diffuse of the three, and the posterior corresponding to the LCM prior of [Manrique-Vallier 2016] is the most concentrated of the three. The posterior corresponding to the log-linear model prior of [King and Brooks 2001], implemented in the `conting` package, is multimodal, which is not unexpected as it is performing Bayesian model averaging (Hoeting et al. 1999) over all hierarchical log-linear models. Due to this multimodality, point estimates (e.g. the posterior mean) may not be reliable summaries of the posterior distribution. We note that all of the credible intervals contain the point estimate of [Spiegel and Salama 2000].
Table 20: Posterior means and 95% credible intervals for \( N \) under each combination of prior for \( N \) and \( \tilde{\pi} \), using the no-highest-order interaction assumption.

|                      | Improper Scale Prior | Negative-Binomial |
|----------------------|----------------------|-------------------|
| Dirichlet            | 18500 [9402, 35908]  | 16051 [9098, 27679] |
| Log-Linear           | 16209 [8731, 30025]  | 14719 [8579, 24878] |
| LCMCR                | 14695 [9423, 23675]  | 14071 [9321, 21604] |
| Conting              | 13000 [9202, 19971]  | 12694 [9175, 19299] |

D.3 A Sensitivity Analysis Probing the Identifying Assumption

We now perform a sensitivity analysis probing the no-highest-order interaction assumption, focusing on the LCM prior for \( \tilde{\pi} \) of Manrique-Vallier (2016) and the negative-binomial prior for \( N \), for concreteness. We fit the model with the identifying assumption described in Section 4.2 varying \( \xi \) over \{1/2, 2/3, 1, 3/2, 2\} (following Gerritse et al., 2015), using the computational approach described in Section 5.2. We emphasize that we only drew samples from \( p_C(\tilde{\pi} | n) \) under the LCM prior for \( \tilde{\pi} \) of Manrique-Vallier (2016) once for both the main analysis in the previous section and the sensitivity analysis described now. This sensitivity analysis is limited in that we followed Gerritse et al. (2015) and chose an arbitrary range of values for \( \xi \) around 1. Due to the difficulty in interpreting the highest-order interaction when there are \( K = 4 \) lists, we are not able to say with confidence whether this range of values is meaningful or not. The posterior density for \( N \) under each identifying assumption is displayed in Figure 5. Posterior means and 95% credible intervals for \( N \) under each identifying assumption combination are displayed in Table 21.

Table 21: Posterior means and 95% credible intervals for \( N \) under each identifying assumption, using the LCM prior for \( \tilde{\pi} \) of Manrique-Vallier (2016) and the negative-binomial prior for \( N \).

| \( \xi \) | Posterior Mean | Credible Interval |
|---------|----------------|-------------------|
| 1/2     | 21476 [13518, 33507] | 17983 [11492, 27987] |
| 2/3     | 14071 [9321, 21604]   | 11121 [7766, 16564]   |
| 1       | 9538 [6943, 13821]    | 9538 [6943, 13821]    |

The results are not very robust to misspecification of \( \xi \) in the chosen range. The credible intervals when \( \xi = 1/2 \) and \( \xi = 2 \) barely overlap. The posterior mean when \( \xi = 2 \) is 32% lower than the posterior mean.
Figure 5: Posterior density of $N$ under each identifying assumption, using the LCM prior for $\hat{\pi}$ of Manrique-Vallier (2016) and the negative-binomial prior for $N$.

when $\xi = 1$ (i.e. under the no-highest-order interaction assumption), and the posterior mean when $\xi = 1/2$ is 53% higher than the posterior mean when $\xi = 1$. The posterior mean $\xi = 1/2$ is more than twice the posterior mean when $\xi = 2$. This lack of robustness to misspecification of $\xi$ would be a cause for concern if the no-highest-order interaction assumption was plausible, and the deviations from the assumption in terms of $\xi$ were also plausible, in the context of the Kosovo data set.

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