Final Project; Categorical Data Analysis

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2019-12-05

1 Estimates of Killing in Casanare

MB: 2 sentences on Casanare

Casanare is a large, rural state in Colombia that includes 19 municipalities and a population of almost 300,000 inhabitants. Located in the foothills of the Andes, Casanare has a history of violence. Multiple armed groups have operated in Casanare including paramilitaries, guerillas and the Colombian military. Many Casanare citizens have suffered violent deaths and disappearances.

AS: 2 sentences on on study/datasets

But *how many* people have been killed or disappeared? We review the Human Rights Data Analysis Group (HRDAG)'s reporting on this work. In this study, the authors used information about victims of killings and disappearances provided by 15 datasets. The datasets come from state agencies – including government, security, forensic and judicial bodies – and from civil society organizations. Across these 15 datasets, there are individuals that have been "captured" only by one dataset, and some that have been captured by multiple. How can we disambguiate the patterns of violence?

2 Multiple Systems Estimation (MSE), Capture Re-Capture

The goal is to estimate the overall population of victims by first estimating the victims who are not captured by any of the datasets. MSE estimates the total number of disappearances by comparing the size of the overlap(s) between lists to the sizes of the lists themselves. If the overlap is small, this implies that the population from which the lists were drawn is much larger than the lists. If, on the other hand, most of the cases on the lists overlap, this implies that the overall population is not much larger than the number of cases listed.

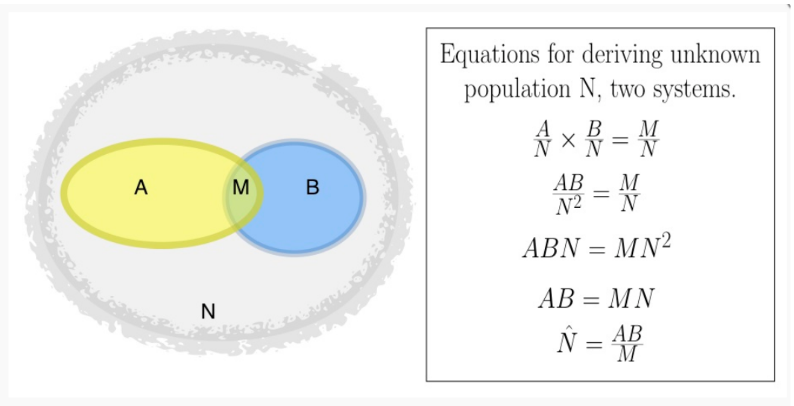

A
M
B
N
Equations for deriving unknown population N, two systems.
$\frac{A}{N} \times \frac{B}{N} = \frac{M}{N}$
$\frac{AB}{N^2} = \frac{M}{N}$
$ABN = MN^2$
$AB = MN$
$\hat{N} = \frac{AB}{M}$

Figure 1: Multiple System Estimation

2.1 MSE Assumptions

There are several MSE assumptions that are need for when there are two "systems" (lists), but not more than that. The assumptions are:

1. *Closed system*: The population of interest does not change during the measurement period. This means that the object of measurement, whether that is a population of persons in a country or a population of violent events that occurred in a state, is a closed system: the target population does not change during the period of measurement. This assumption is generally unproblematic for data on violent events, because events that occurred cannot "un-occur" later.

2. *Perfect matching (record linkage!)*: The overlap between systems (i.e., the group of cases recorded in more than one list) is perfectly identified.

3. *Equal probability of capture*: For every data system, each individual has an equal probability of being captured. For example, every death has probability X of being recorded in list 1, every death has probability Y of being recorded in list 2, and so on. TThis assumption, the homogeneity of capture probability, is unlikely to hold for any type of violence data. For example, persons with fewer social connections may be both more likely to go missing and less likely to be reportedmissing; rural locations are more difficult to access than urban ones. Constructing two-sample estimates without accounting for different probabilities of capture leads to conclusions that may be biased.

4. *Independence of lists*: Capture in one list does not affect probability of capture in another list. For example, being reported to one NGO does not change the probability that an individual is reported to another. The third assumption, independence of systems, is similarly difficult to meet.

Like differences in capture probability, dependences between systems are impossible to account for in the the two-system setting. A common example here is the difference between governmental and non-governmental organizations. Because different populations may have different levels of trust in the two organizations, reporting to one type of organization may imply that the witness is very unlikely to report to the other.

3 Overview of Data

Table 1: Contingency Table

	Organization	Total Captures	Unique	Type
d_CCJ.n	Colombian Commision of Jurists	214	48	judicial
d_EQU.n	Equitas	22	0	civil
d_FON.n	Fondelibertad	304	67	security
d_IMLD.n	National Institute of Forensic Medicine Disappearances	153	9	forensic
d_PN0.n	Policía Nacional	825	221	security
d_CIN.n	CINEP	267	91	civil
d_FAM.n	Families of Victims' Organizations	51	1	civil
d_FSR.n	Prosecutor General of Santa Rosa	151	0	security
d_IMLM.n	Instituto Nacional de Medicina Legal	1878	1219	forensic
d_VP.n	Vice Presidency Office	501	284	judicial
d_CCE.n	Colombia-Europe	72	30	civil
d_CTI.n	Technical Investigative Body of the Prosecutor Generals Office	36	0	judicial
d_FDC.n	Prosecutor General list of the Disappeared	623	376	forensic
d_GAU.n	Gaula	110	1	security
d_PL.n	Pais Libre	9	0	civil

3.1 Overall Trends

The following graph shows that violence has been concentrated in municipality. We can see that the *reported* violence (i.e. the counts in the 15 datasets) appears to have intensified across all municipalities in Casanare in 2003-2004 and then dropped.

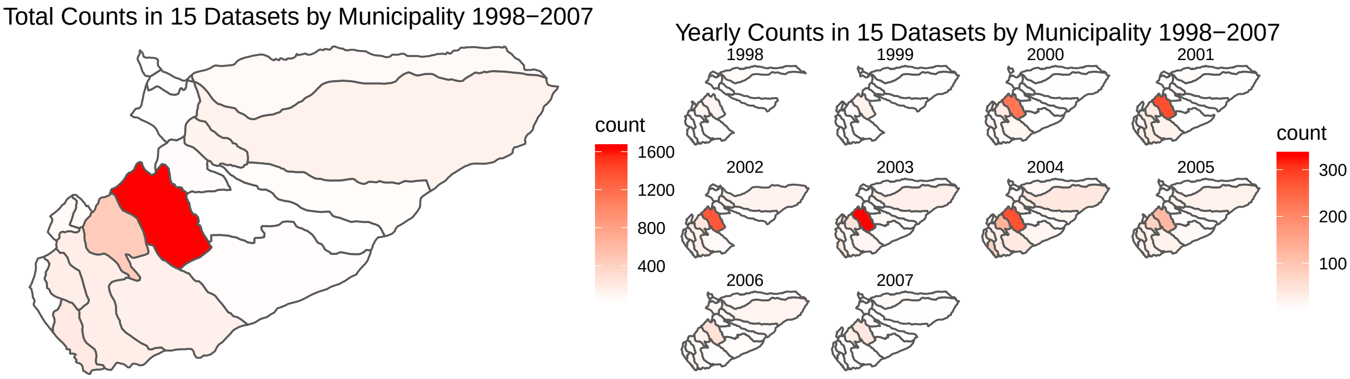

Total Counts in 15 Datasets by Municipality 1998−2007
count
1600
1200
800
400
Yearly Counts in 15 Datasets by Municipality 1998−2007
1998
1999
2000
2001
2002
2003
2004
2005
2006
2007
count
300
200
100

Figure 2: Overall Trends in 15 Datasets by Municipality

Looking just at the the totals of the 15 datasets and individual may think that the violence peaked in 2003-2004 and the total of victims is 3000? However, just looking at the trends amoung the totals of the 15 datasets does not give the whole picture.

3.1.1 Heterogenity Issues

AS: looking at certain year and show total, and lista, listb, listc to show diff probs

3.2 Different Datasets - Different Stories

We motivate our need for a more sophisticated analysis by showing the reporting patterns of 3 different organizations across 1998-2007. If we relied on just one organization or even a combination of two we could tell diffent stories regarding the violence. Relying on FAM shows a peak in violent incidents in 2003, while reports by IMLM show a peak in 2004 . Using multiple systems estimation allows us to parse both the reported and unreported violent in Casanare.

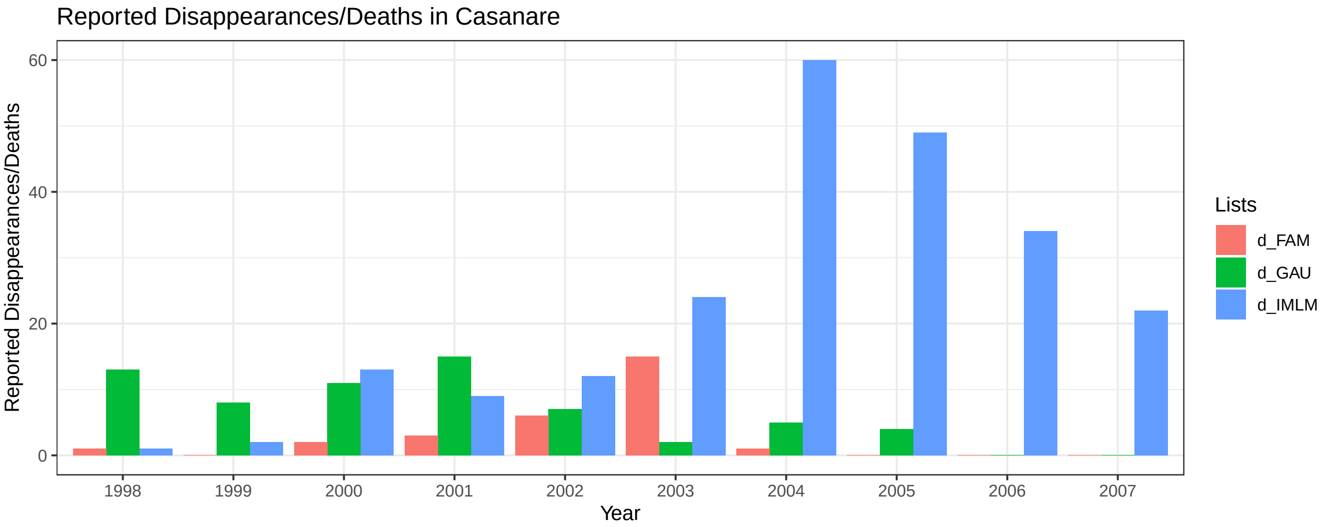
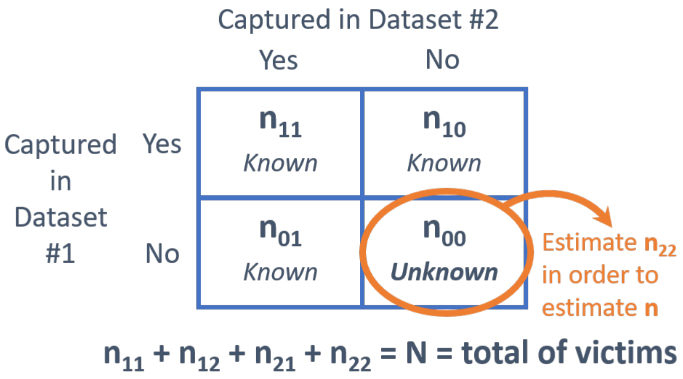


Figure 3: Count Trends for Three Organizations

4 Loglinear Modelling

In order to do our estimation, we will use loglinear modeling. We will describe the model as if we had two datasets (for simplicity). We know the victims "captured" by only dataset 1, only dataset 2, and both datasets. However, we don't know the amount of victims that are not captured by either list. Estimate this value allows us to estimate the total count of victims.



		Captured in Dataset #2	
		Yes	No
Captured in Dataset #1	Yes	n_{11} *Known*	n_{10} *Known*
	No	n_{01} *Known*	n_{00} ***Unknown***

Estimate n_{22} in order to estimate **n**

$$n_{11} + n_{12} + n_{21} + n_{22} = N = \text{total of victims}$$

The count of victims captured into a dataset or combindation of datasets is n_{11}, n_{10}, n_{01}, and n_{00}. Each of these cells is a count of victims captured. The subscripts denote which datasets a victim has been captured. The subscripts denotes if the victim has been captured (1), or not been captured by a certain data set. For n_{ij}, i is for dataset #1 and j is dataset #2.

Our estimates are primarily based on Poisson regression. Poisson regression treaets these cell counts - not the underlying individual cases data

4.1 Estimating the Total Count of Victims

We are interested in estimating n_{00}, which also allows us to estimate the total number of victims.
The (log of the) expected cell count n_{00} is a function of the other observed cell counts, as shown in the equation below.

$$\log(n_{00}) = \alpha + \beta_1 \cdot \mathbb{1}(x \in n_{10}) + \beta_2 \cdot \mathbb{1}(x \in n_{01})$$

This is the saturated form of the log-linear models introduced in Bishop, Fienberg and Holland (1975). To quote from Agresti, "the saturated GLM has a separate parameter for each observation. It gives a perfect fit. This sounds good, but it is not a helpful model. It does not smooth the data or have the advantages that a simpler model has, such as parsimony. Nonetheless, it serves as a baseline for other models, such as for checking model fit."

When estimation of the total "population" of missing people in Casanare is the goal (as it typically is with multiple-systems estimation), the key value here is the intercept α. To estimate $\log(n_{00})$, all the other values in the model are zero, as the indicator functions for n_{ij} for zero. Therefore the only term that contributes to the estimate of $\log(n_{00})$ is α. The value of n_{00} is therefore the exponentiated value of a, that is, $\exp(\alpha)$. The total number of cases, N, is the sum of the observed cases plus $\exp(\alpha)$.

$$\begin{aligned}
\log(n_{00}) &= \alpha \underbrace{+\beta_1 \cdot \mathbb{1}(x \in n_{10}) + \beta_2 \cdot \mathbb{1}(x \in n_{01})}_{\text{each } = 0} \\
\log(n_{00}) &= \alpha \\
\hat{n}_{00} &= \exp\{\hat{\alpha}\} \\
\\
\hat{N} &= n_{11} + n_{10} + n_{01} + \hat{n}_{00}
\end{aligned}$$

As with any regression and data mining model, we want to avoid overfitting. There is a tradeoff we need to balance between "goodness of fit", and simple (parsimonious) models.

We need to find the best model in order to get an accurate estimate of α. Thus, we should determine whether the full (saturated) model above, which assumes that all three two-way interactions between datasets are important, is actually necessary. There is one simpler models that assume the two-way interaction.

$$\log(n_{00}) = \alpha + \beta_1 \cdot \mathbb{1}(x \in n_{10}) + \beta_2 \cdot \mathbb{1}(x \in n_{01}) + \beta_{12} \cdot \mathbb{1}(x \in n_{11})$$

In this case, we can clearly write out the possible model. During model selection, we estimate these models and choose the model that minimizes the Bayesian Information Criterion (BIC), a test that weighs goodness of fit against degrees of freedom.

4.2 Challenges with Loglinear models

1. **Interpretation:** The inclusion of so many variables in loglinear models often makes interpretation very difficult.

2. **Independence Assumption:** The frequency in each cell is independent of frequencies in all other cells, which is not necessarily the case here. We attempt to model this.

3. **Sample Size Requirement:** With loglinear models, you need to have at least 5 times the number of cases as cells in your data. If you do not have the required amount of cases, then you need to increase the sample size or eliminate one or more of the variables.

4.3 Choosing our "Systems"

Our dataset encompasses 15 datasets, far too many to model with a loglinear model. We collapse these 15 datasets into 4 systems (i.e. groups) based on the type of organization that produced the dataset.

Table 2: Example of Information from Systems

security_ind	forensic_ind	judicial_ind	civil_ind	Freq
0	0	0	1	5
0	0	1	0	1
0	0	1	0	1
1	0	0	0	1
1	0	1	0	1
0	0	1	1	1

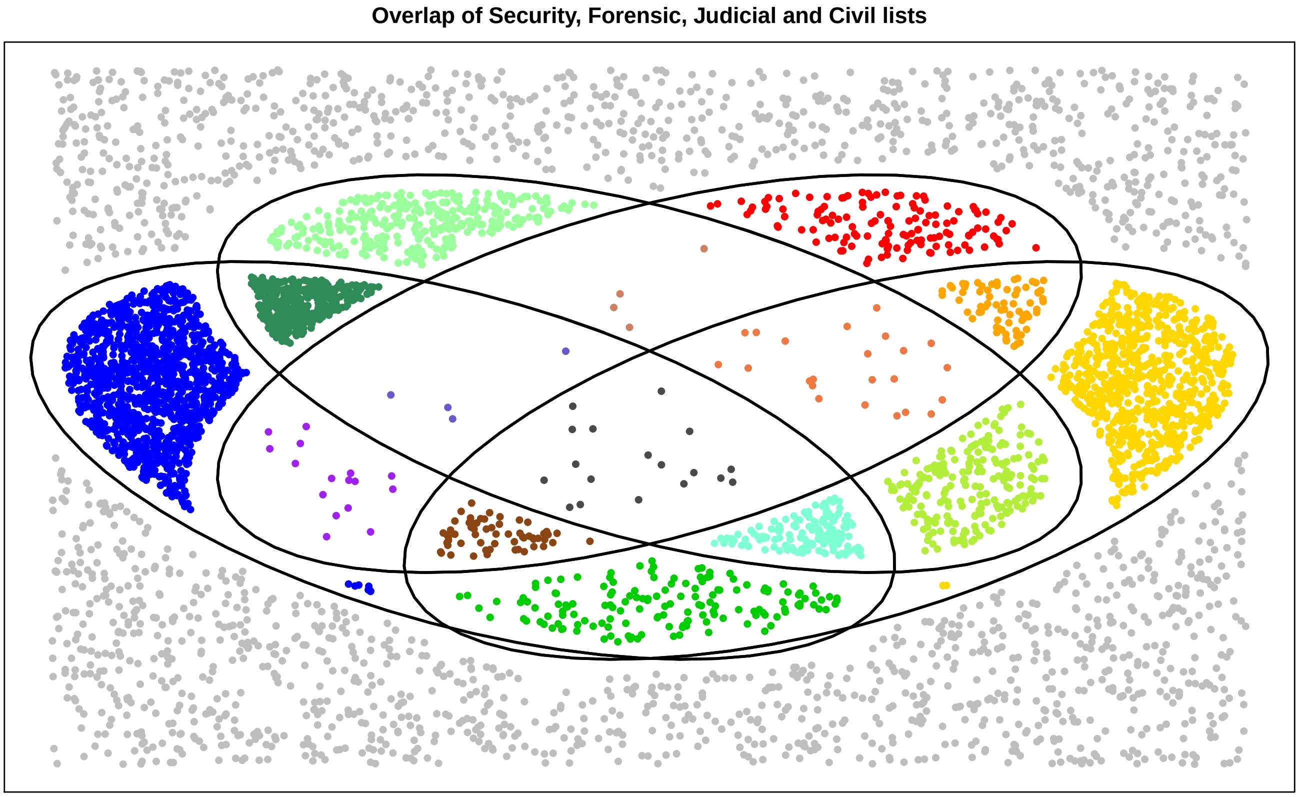


Figure 4: Estimated Venn Diagram of Systems

In the above Venn Diagram, the colored dots represent a specific victim. We are trying to estimate the victims that are not caputred in one of th lists (shown by the graph dots). We can see there is not a lot of overlap, which suggests there may be lack of heterogenity capture probability (i.e. the probability of a victim captured differs from list to list). In addition, this implies that there is likely a much larger population of victims than counted in the 15 datasets.

4.4 Model Definitions

4.4.1 Types of Models

Models will be donoted by M, and the subscripts will denote the type of model.

- M_0: The M_0 model is the simplest possible multiple source capture recapture model. It assumes that there is no heterogeneity and that all lists (civil, security, judicial, etc) have the same probability of capturing individuals. We know that this is not the case here.

- M_t: This model relaxes the M_0 model to allow for lists to have different capture rates.
- M_h: This model relaxes the M_0 model to allow for individual capture heterogeneity.
- M_{th}: This model allows for both list heterogeneity and capture events having different rates.

4.4.2 Types of Heterogeniety

When heterogeneity in capture probability is present (i.e. the probability of a list capturing a victims differs), there are different forms that this heterogeneity can take.

- Normal: The log odds of capture follows a Normal distribution.
- Darroch: The log odds of capture among those who were not captured follows a Normal distribution.
- Poisson: The log odds of capture among those who were not captured follows a Poisson distribution.
- Gamma: The log odds of capture among those who were not captured follows a Gamma distribution.

4.5 Non-Hierarchical Models

After collapsing the 15 lists into four systems, we fit several loglinear models. We see that the best fits clearly take into account both system and individual heterogeneity. We therefore choose the M_{th} model with the log odds of capture among those who were not captured follows a Gamma distribution. We see that the M_0 model demonstrates a clear lack of fit, which we would expect for this data. The models listed below are *not* hierchachal in nature.

We will need the hierchachal structure to perform model selection. It's important to note that a model is not chosen if it bears no resemblance to the observed data. The choice of a preferred model is typically based on a formal comparison of goodness-of-fit statistics associated with models that are related hierarchically (models containing higher order terms also implicitly include all lower order terms). Ultimately, the preferred model should distinguish between the pattern of the variables in the data and sampling variability, thus providing an intuitive interpretation.

The "number of captured units" is the number of observed elements, in this example, the number of people documented as missing/killed, we usually call this N_c (N for overall total, and c denoting caputred. The "abundance" column shows the estimate of $\hat{N}$, the total population including the observed and the estimated unobserved deaths. The AIC and BIC columns show the "information coefficients" which balance the goodness of fit (shown in the "deviance" column) with the information used to estimate the model (degrees of freedom indicate this). Model selection often occurs based on the smallest AIC and BIC values, however this can only be done with hierchical models which is not the case here.

Table 3: Summary of Models (Non-hierarchical models)

	abundance	stderr	deviance	df	AIC	BIC	infoFit
M0	5604.929	100.60691	2279.4707	13	2376.7355	2389.0571	0
Mt	5232.814	87.30936	529.8227	10	633.0875	663.8915	0
Mh Chao (LB)	5970.687	139.89294	2253.9791	12	2353.2439	2371.7263	0
Mh Poisson2	6147.489	188.43134	2262.1217	12	2361.3865	2379.8689	0
Mh Darroch	6866.486	367.88961	2257.9368	12	2357.2016	2375.6840	0
Mh Gamma3.5	7725.102	634.44312	2256.6358	12	2355.9007	2374.3831	0
Mth Chao (LB)	5665.285	125.06924	473.7645	8	581.0293	624.1550	0
Mth Poisson2	6035.010	181.67803	482.2671	9	587.5319	624.4967	0
Mth Darroch	7204.688	411.30447	476.0572	9	581.3221	618.2869	0
Mth Gamma3.5	8782.672	810.69350	474.7154	9	579.9802	616.9450	0
Mb	4228.193	64.66437	2107.1837	12	2206.4485	2224.9309	0
Mbh	3643.007	47.70713	1618.9871	11	1720.2520	1744.8952	0

Each model controls for a subset of all the possible interactions among the models. In the context of MSE, the two- and three-way interactions estimate (and to some extent, control for) associations in the probabilities of capture between (and among) the lists. For example, is a certain person more likely to be seen on one list, and also more likely to be seen on a second list? If associations like this are present (and they usually are), they can bias the estimate.

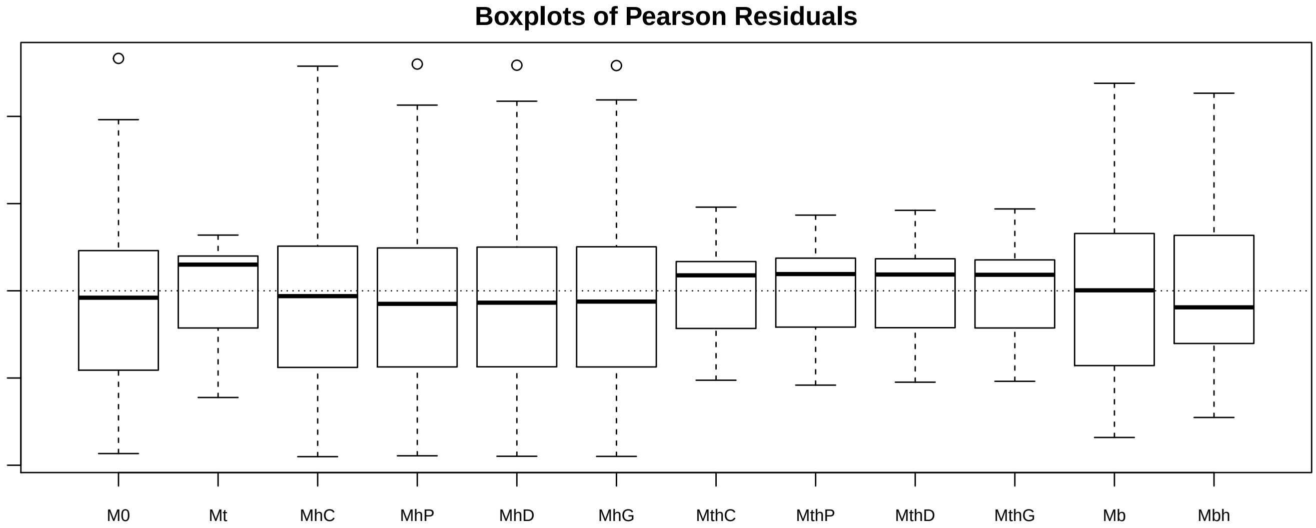


Figure 5: Boxplot of Residuals for Models

These boxplots of residuals offer a general assesment of model fit. The light dotted line represents zero, and ideally you want the residuals centered around zero. We see that there is significantly less variation in the M_{th} Models. These models account for list heterogenity (probability of capture for a specific victim varies from list to list) and individual heterogenity (probability of capture for a specific list varies from victim to victim). Models that account for heterogenity offer less variation but also do not have residuals centered at zero.

4.6 Specific Model Results

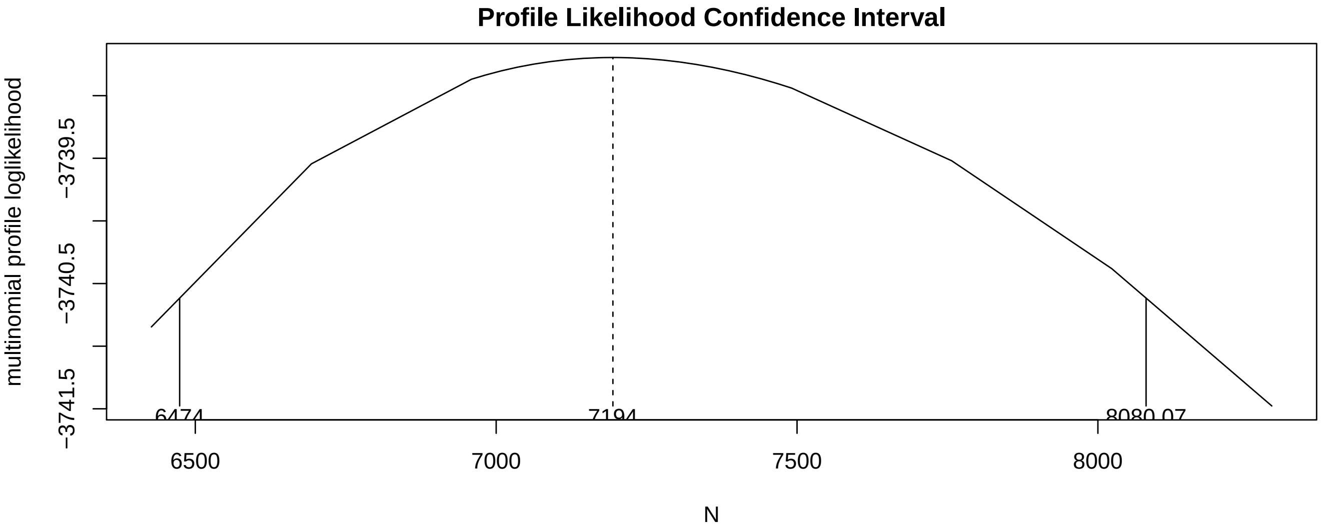


Figure 6: Profile Likelihood of Specific Model

Table 4: Confidence Interval of Specific Model

	abundance	InfCL	SupCL
Mth Darroch	7194	6474	8080.07

4.7 Capture Recapture

We display some basic capture-recapture frequency statistics to explore capture patterns. It displays, for $i = 1, ...t$, the number of people captured i times (f_i), the number of people captured for the first time on occasion i (u_i), the number of units capturedfor the last time on occasion i (v_i) and the number of units captured on occasion i (n_i). If the n_i statistics vary among capture occasions, there is a temporal effect– which we clearly see here. We would expect the top panel of the plot to be linear, while the bottom panel should be concave down or exhibit no pattern for capture patterns that are best fit with M_{th} models.

```
##
## Number of captured units: 3501
##
## Frequency statistics:
##         fi    ui    vi    ni
## i = 1  2392  1128   317  1128
## i = 2   866  1455  1640  2028
## i = 3   225   785  1216  1387
## i = 4    18   133   328   328
## fi: number of units captured i times
## ui: number of units captured for the first time on occasion i
## vi: number of units captured for the last time on occasion i
## ni: number of units captured on occasion i
```

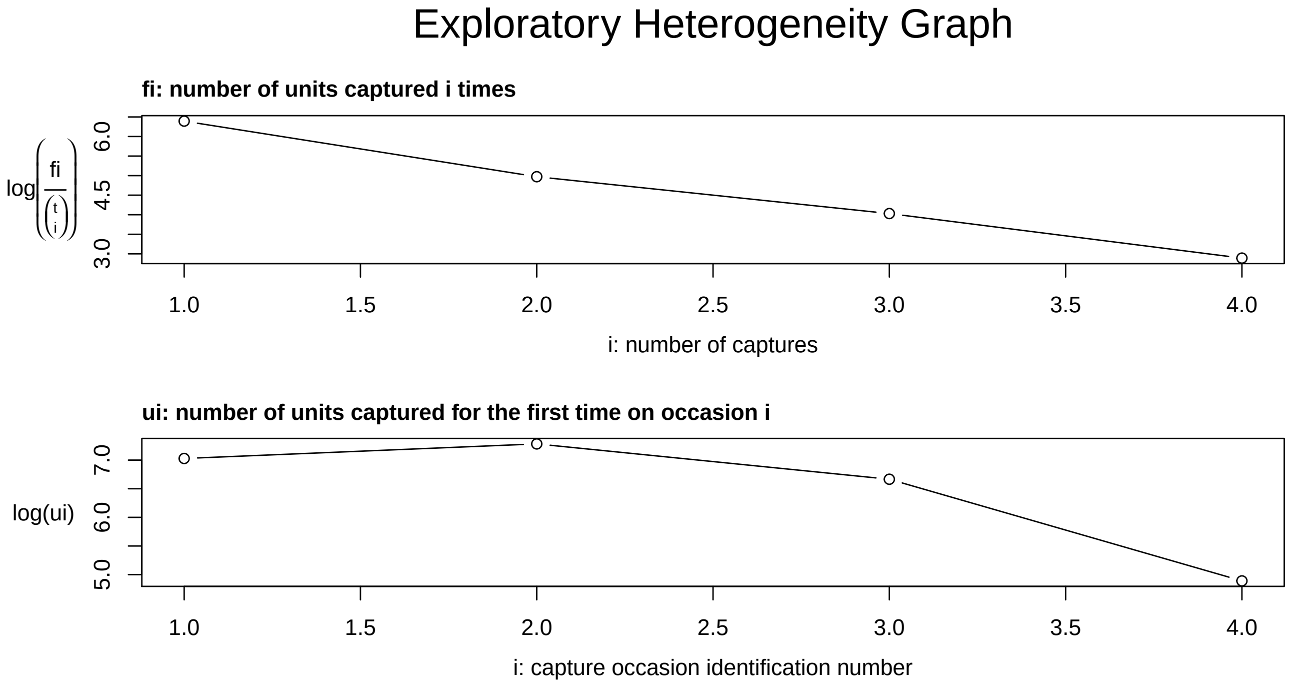


Figure 7: Capture-Recapture Frequency Statistics

$$\log\left(\frac{f_i}{\binom{t}{i}}\right) = \log\left(\frac{N \times P(i \text{ captures})}{\binom{t}{i}}\right) = \log(N(1-p)^{t-i}p^i = \log(N(1-p)^t) + i\log\left(\frac{p}{1-p}\right)$$

4.8 Hierarchical Models: Choosing a Model

The iterative proportional fitting process generates maximum likelihood estimates of the expected cell frequencies for a hierarchical model. In short, preliminary estimates of the expected cell frequencies are successfully adjusted to fit each of the marginal sub-tables specified in the model.

AS: wants to rewrite
For example, in the model $list_1$, $list_{12}$, $list_{123}$, the initial estimates are adjusted to fit $list_{12}$ then $list_{23}$ and finally to equal the $list_{123}$, observed frequencies. The previous adjustments become distorted with each new fit, so the process starts over again with the most recent cell estimate. This process continues until an arbitrarily small difference exists between the current and previous estimates.

We fit hierchachal models, restricting to second-order (no three-way interactions) for sake of interpretation.The best model according to the BIC criteria, is below: estimates a total for missing/disappeared people as 8607, which is similar to the 8782 than that of the non-hierch., interactionless, model.

The below describes three possible models. The $\log(\hat{N})$ is based on the grand mean μ and effects based on our 4 systems (which are represented by λ). The subscripts of λ denote whether the effect is coming from a single system or the overlap between two systems (note we did not look at models that more than two-way interactions).

$$\begin{aligned} \text{Top Model:} \quad & \log(\hat{N}) = \mu + \lambda_{12} + \lambda_{13} + \lambda_{14} + \lambda_{23} + \lambda_{24} + \lambda_{34} \\ \text{Example of Middle Model:} \quad & \log(\hat{N}) = \mu + \lambda_{13} + \lambda_{14} + \lambda_{24} \\ \text{Bottom Model:} \quad & \log(\hat{N}) = \mu + \lambda_1 + \lambda_2 + \lambda_3 + \lambda_4 \end{aligned}$$

Table 5: ’Top’ Five, ’Middle’ Five, and ’Bottom’ Five Models (Hierarchical models)

	abundance	stderr	bias	deviance	df	AIC	BIC	infoFit
12,13,14,23,24,34	8817.112	1515.7607	237.8220039	72.33182	3	189.5966	263.5263	0
12,13,14,23,24	5076.249	168.5601	9.6710160	93.42304	4	208.6879	276.4567	0
12,13,14,23,34	7308.085	455.7503	36.3107669	73.99807	4	189.2629	257.0317	0
12,13,14,24,34	8695.570	493.7868	32.6905220	72.33923	4	187.6040	255.3729	0
12,13,23,24,34	9267.442	876.2745	91.6873828	72.44539	4	187.7102	255.4791	0
12,24,34	6990.394	275.9882	8.1501334	251.01919	6	362.2840	417.7312	0
13,14,23	5388.545	160.4725	6.9759022	180.47969	6	291.7445	347.1917	0
13,14,24	6408.681	225.7425	8.3355958	397.52853	6	508.7934	564.2406	0
13,23,24	5052.802	130.3749	3.2161351	209.76658	6	321.0314	376.4786	0
13,23,34	5178.863	140.5477	3.1073571	223.51518	6	334.7800	390.2272	0
14,2,3	6349.780	217.6530	6.4628534	444.04882	8	551.3136	594.4393	0
23,1,4	5076.432	127.2073	1.1770391	278.46874	8	385.7336	428.8592	0
24,1,3	6089.940	188.3562	2.6692553	450.63028	8	557.8951	601.0207	0
34,1,2	5903.270	172.5871	1.4531676	404.10047	8	511.3653	554.4909	0
1,2,3,4	6035.010	181.6780	0.7620688	482.26705	9	587.5319	624.4967	0

We also plot the BIC values for different models and their accompanying estimates of $\hat{N}$.

Note that these the hierch. models have different estimates ,ranging from 5231 to 8607, all within very similar BIC values Which one should we use?

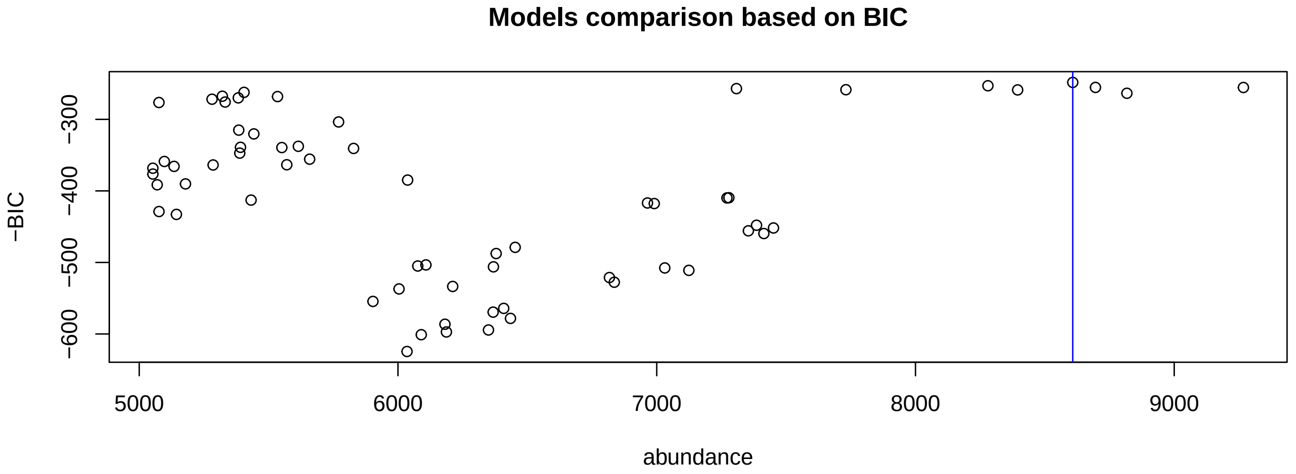


Figure 8: Hiercharical Models BIC Plot

This is the fundamental problem of the frequentist approach. We could just pick the “best” model, i.e., the one with the lowest BIC. Unfortunately, just picking one model ignores the error that we introduce by the selection itself. It also forces us to decide which dependencies among the systems we will control for, forcing us to decide which dependencies will not be included in the model.

5 Goodness of Fit

AS

I will describe here how likelihood ratio test is better for model comparison than Pearson's Chi-square??

6 Conclusions

MB

- total under 15 datasets 3000 (? check this number)
- Lots of uncertaintiy (not even sure our data meets requirements for modeling)
- "valid" estimates can range from 5000 - 9000 (could be used for different political stories)