Base Model Specification

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Notation and Assumptions

Our notation and assumptions closely follow that of Sadinle (2017). Denote two files as \mathbf{X}_A and \mathbf{X}_B , with n_A and n_B records respectively, and with records indexed as $i \in \{1, \dots, n_A\}$ in \mathbf{X}_A and $j \in \{1, \dots, n_B\}$ in \mathbf{X}_B . Without loss of generality, label the files such that $n_A \geq n_B$. We also assume there are no duplicates within files, only across. For each record pair under consideration, we generate a comparison vector $\gamma_{ij} = \{\gamma_{ij}^1, \dots, \gamma_{ij}^F\}$, where F is the number of fields used in the linkage and each takes γ_{ij}^f takes on a value $l \in \{1, \dots, L_f\}$ indicating level agreement between the two records on a specified field.

Following the Fellegi Sunter framework, we define $m^{fl} := P(\gamma_{ij}^f = l | Z_j = i)$ to be the probability of observing agreement level l in field f for records i and j given that the records are a match, and similarly define $u^{fl} := P(\gamma_{ij}^f = l | Z_j \neq i)$, for non-matches. We denote λ to be the (marginal) probability that some record $j \in \mathbf{X}_B$ has a match in \mathbf{X}_A .

Lastly, we adopt from Sadinle 2017 the matching labelling $\mathbf{Z} = (Z_1, \dots, Z_{n_A})$, defined as

$$Z_j = \begin{cases} i, & \text{if records } i \in \mathbf{X}_A \text{ and } j \in \mathbf{X}_B \text{ refer to the same entity;} \\ n_A + 1, & \text{if record } j \in \mathbf{X}_B \text{ does not have a match in file} \mathbf{X}_B; \end{cases}$$

Wherever possible, we reserve superscripts for denoting field, level, and linkage cluster, and reserve subscripts for record indices. For example, $\mathbf{m}^f = (m^{f1}, \dots, m^{fL_f})$ is the probability distribution governing field f for matching records, and $\mathbf{m}_{ij} = \prod_{f=1}^{L_f} \prod_{l=1}^{L_f} (m^{fl})^{\gamma_{ij}^f = l} = P(\gamma_{ij}|Z_j = i)$ is product of the relevant of the appropriate \mathbf{m} parameters for record pair (i,j). We hope that these conventions avoid overloaded notation in the likelihood and subsequent derivations.

Model Specification

Additionally, our model differs from that of Sadinle 2017 through its explicit dependence on a beta random variable λ that models the rate of matching across records. Sadinle marginalizes over such a random variable in his derivations of the "beta prior for bipartite matching," but here we provide derivations without marginalizing in order to specify differing rates of matching for different linkage clusters.

Prior Distributions and Likelihood

For fields $f \in \{1, ..., F\}$ and levels $l \in \{1, ..., L_f\}$ we adopt the following likelihood and prior distributions. Note that likelihood is related to that of Sadinle (2017), but includes dependence on the λ random variable. It also makes it explict that units of observation under this model are the n_B records in \mathbf{X}_B , a crucial distinction when compared to the likelihood over the $n_A \times n_B$ record pairs in the original Fellegi Sunter model.

$$P(\Gamma | \mathbf{Z}, \mathbf{m}, \mathbf{u}, \lambda) = \prod_{j=1}^{n_B} \prod_{i=1}^{n_A} \mathbf{m}_{ij}^{\mathbf{1}_{z_j = i}} \mathbf{u}_{ij}^{\mathbf{1}_{z_j \neq i}}$$
 $\mathbf{m^f} \sim \mathrm{Dirichlet}(\alpha^{f1}, \dots, \alpha^{fL_f})$
 $\mathbf{u^f} \sim \mathrm{Dirichlet}(\beta^{f1}, \dots, \beta^{fL_f})$
 $Z_j | \lambda = \begin{cases} \frac{1}{n_A} \lambda & z_j \leq n_A; \\ 1 - \lambda & z_j = n_A + 1 \end{cases}$
 $\lambda \sim \mathrm{Beta}(\alpha_\lambda, \beta_\lambda)$

The prior for Z_j has equal probability of matching to all records $i \in \mathbf{X}_A$, and non-matching probability governed by λ . Therefore a $\lambda \sim \mathrm{Beta}(1,1)$ corresponds to a prior belief that nonmatches and matches are equally likely, and a $\lambda \sim \mathrm{Beta}(1,\frac{1}{n_A})$ prior corresponds to a uniform prior on the labelling of \mathbf{Z} .

Posterior Sampling

We work with the following factorization of the joint distribution:

$$p(\Gamma, \mathbf{Z}, \mathbf{m}, \mathbf{u}, \lambda) = p(\Gamma | \mathbf{Z}, \mathbf{m}, \mathbf{u}) p(\mathbf{Z} | \lambda) p(\mathbf{m}, \mathbf{u}) p(\lambda)$$

This factorization leads to following Gibbs Sampler:

Sample $\mathbf{m}^{(s+1)} \mathbf{u}^{(s+1)} | \Gamma, \mathbf{Z}^{(s)}$: The \mathbf{m} and \mathbf{u} parameters are updated through standard multinomial-dirichlet mechanics. Thus we have

$$\begin{split} \mathbf{m^f}|\mathbf{Z}, \Gamma \sim \text{Dirichlet}(\alpha^{f1}(\mathbf{Z}), \dots, \alpha^{fL_f}(\mathbf{Z})) \\ \mathbf{u^f}|\mathbf{Z}, \Gamma \sim \text{Dirichlet}(\beta^{f1}(\mathbf{Z}), \dots, \beta^{fL_f}(\mathbf{Z})) \end{split}$$
 where $\alpha_{fl}(\mathbf{Z}) = \sum_{i,j} I_{obs}(\gamma^f_{ij}) \mathbf{1}_{\gamma^f_{ij} = l} \mathbf{1}_{z_j = i}$ and $\beta_{fl}(\mathbf{Z}) = \sum_{i,j} I_{obs}(\gamma^f_{ij}) \mathbf{1}_{\gamma^f_{ij} = l} \mathbf{1}_{z_j \neq i}.$

\underline{Sample $\lambda^{(s+1)}|\mathbf{Z}^{(s)}$ As a function of λ , the linkage structure parameter \mathbf{Z} is sequence of successes (when $z_j < n_A + 1$) and failures (when $z_j = n_A + 1$), and therefore

 $p(\mathbf{Z}|\lambda) = \mathcal{L}(\lambda|\mathbf{Z})$ is determined only by the number of dupliates $D = \sum_{i=1}^{n_B} \mathbf{1}_{z_j < n_A + 1}$ encoded by \mathbf{Z} . Thus we have

$$p(\lambda|\mathbf{Z}) \propto p(\mathbf{Z}|\lambda)p(\lambda)$$

$$\propto \lambda^{D} (1-\lambda)^{n_{B}-D} \lambda^{\alpha_{\lambda}-1} (1-\lambda)^{\beta_{\lambda}-1}$$

$$\propto \lambda^{D+\alpha_{\lambda}-1} (1-\lambda)^{n_{B}-D+\beta_{\lambda}-1}$$

$$\implies \lambda^{(s+1)}|\mathbf{Z}^{(s+1)} \sim \text{Beta}(D+\alpha_{\lambda}, n_{B}-D+\beta_{\lambda})$$

Sample $\mathbf{Z}^{(s+1)}|\Gamma, \mathbf{m}^{(s+1)}, \mathbf{u}^{(s+1)}, \lambda^{(s+1)}$ Because we sample Z_j independently of all other $Z_{j'}$, we use only the full conditional for an individual Z_j . Let $\Gamma_{.j}$ denote the set of n_A comparison vectors with $j \in B$, and note that as a function of Z_j , the likelihood $p(\Gamma_{.j}|Z_j, \mathbf{m}, \mathbf{u})$ is a discrete distribution with probabilities proportional to

$$p(\Gamma_{.j}|Z_j = z_j, \mathbf{m}, \mathbf{u}) \propto \prod_{i=1}^{n_A} \mathbf{m}_{ij}^{\mathbf{1}_{z_j = i}} \mathbf{u}_{ij}^{\mathbf{1}_{z_j \neq i}}$$

$$\propto \prod_{i=1}^{n_A} \left(\frac{\mathbf{m}_{ij}}{\mathbf{u}_{ij}}\right)^{\mathbf{1}_{z_j = i}} \quad \text{Divide through by } \prod_{i=1}^{n_A} \mathbf{u}_{ij}$$

$$= \begin{cases} w_{ij} & z_j \leq n_A; \\ 1 & z_j = n_A + 1 \end{cases}$$

where $w_{ij} = \frac{\mathbf{m}_{ij}}{\mathbf{u}_{ij}} = \frac{P(\gamma_{ij}|Z_j=i)}{P(\gamma_{ij}|Z_j\neq i)}$. The interested reader should note that these are precisely the likelihood ratios used in the Fellegi-Sunter model to classify matches and non-matches, and we therefore refer to w_{ij} as the *Fellegi Sunter weights*.

 $p(Z_i|\Gamma_i, \mathbf{m}, \mathbf{u}, \lambda) \propto p(\Gamma_i|Z_i, \mathbf{m}, \mathbf{u})P(Z_i|\lambda)$

With the likelihood in this form, we can derive the full conditional

$$\propto \left(\sum_{i=1}^{n_A} w_{ij} \mathbf{1}_{z_j=i} + \mathbf{1}_{z_j=n_A+1} \right) \left(\lambda \sum_{i=1}^{n_A} \frac{1}{n_A} \mathbf{1}_{z_j=i} + (1-\lambda) \mathbf{1}_{z_j=n_A+1} \right) \\
= \frac{\lambda}{n_A} \sum_{i=1}^{n_A} w_{ij} \mathbf{1}_{z_j=i} + (1-\lambda) \mathbf{1}_{z_j=n_A+1}$$

$$\implies Z_j^{(s+1)}|\mathbf{m},\mathbf{u},\Gamma,\lambda \propto \begin{cases} \frac{\lambda}{n_A}w_{ij} & z_j \leq n_A; \\ 1-\lambda & z_j = n_A+1 \end{cases}$$

Here, one should note that if we choose to integrate over the posterior of λ and rearrange

terms, we produce the following sampling mechanism:

$$Z_j^{(s+1)}|\mathbf{m}, \mathbf{u}, \mathbf{Z}^{(\mathbf{s})} \propto \begin{cases} w_{ij} & z_j \leq n_A; \\ n_A \frac{n_B - D + \beta_\lambda}{D + \alpha_\lambda} & z_j = n_A + 1 \end{cases}$$