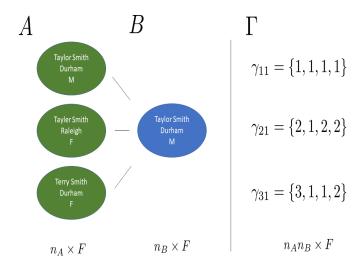
# Efficient and Scalable Bipartite Matching through Fast Beta Linkage (fabl)

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# Introduction to Record Linkage

## Fellegi and Sunter



#### Notation

- ▶ File A with records indexed  $i \in \{1, ..., n_A\}$  and file B with records  $j \in \{1, ..., n_B\}$ . We use F features for linkage, with  $L_f$  possible levels of agreement on feature f.
- ho  $\Gamma \in \mathbb{R}^{n_A n_B imes F}$  matrix of comparison vectors where  $\gamma_{ij}^f \in \{1, \dots, L_f\}$
- $Z_j = \begin{cases} i, & \text{if records } i \in A \text{ and } j \in B \text{ refer to the same entity;} \\ n_A + 1, & \text{if record } j \in B \text{ does not have a match in file } A; \end{cases}$
- $\qquad \qquad \mathbf{u}_{fl} = P\left(\gamma_{ij}^f = I | Z_j \neq i\right)$

m's and u's

#### Previous work

- ► Fellegi and Sunter (1969)
  - independent classification of all  $n_A n_B$  record pairs. Transitive closure acheived through postprocessing
- ► Enamorado et al (2019): fastlink
  - provides efficient and scalable FS model
- ► Sadinle (2017) Beta Record Linkage (BRL)
  - Bayesian method for bipartite matching, strictly enforces one-to-one matching. Does not scale well to large linkage tasks

# Fast Beta Linkage (fabl)

$$P(\Gamma | \mathbf{Z}, \mathbf{m}, \mathbf{u}) = \prod_{j=1}^{n_B} \prod_{i=1}^{n_A} \left[ \prod_{f=1}^F \prod_{I=1}^{L_f} m_{fI}^{I(Z_j=i)} u_{fI}^{I(Z_j\neq i)} \right]^{I(\gamma_{ij}^f=I)}$$

$$\mathbf{m_f} \sim \mathsf{Dirichlet}(\alpha_{f1}, \dots, \alpha_{fL_f})$$

$$\mathbf{u_f} \sim \mathsf{Dirichlet}(\beta_{f1}, \dots, \beta_{fL_f})$$

$$Z_j | \lambda = \begin{cases} \frac{1}{n_A} \lambda & z_j \leq n_A; \\ 1 - \lambda & z_j = n_A + 1 \end{cases}$$

$$\lambda \sim \mathsf{Beta}(\alpha_{\lambda}, \beta_{\lambda})$$

 Model specification allows for parallel/distributed computing, hashing of comparison vectors, and storage efficient indexing (SEI)

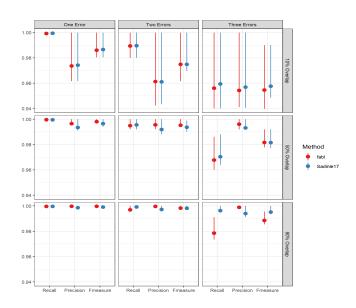
## Hashing

- ▶ Recognize there are at most  $P = \prod_{f=1}^F L_f$  unique agreement patterns. When (i,j) pair exhibits agreement pattern p, say  $(i,j) \in h_p$
- Reduce data to sufficient statistics
  - $H_p = \sum_{i,j} \mathbf{1}_{(i,j) \in h_p}$
  - $H_{p_j} = \sum_{i} \mathbf{1}_{(i,j) \in h_p}$
- ▶ Gibbs sampler over each record pair has complexity  $O(n_A \times n_B \times F)$ , but sampler over agreement pattern has complexity  $O(P \times n_B \times F)$
- Speeds up posterior calculations and sampling

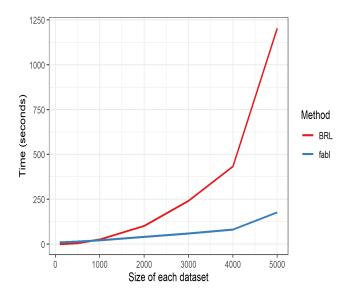
## Managing Large Data

- ▶ **Distributed Computing** Partition data in to chunks  $\{A_I\}$  and  $\{B_J\}$ . Compare records, hash results, compute summary statistics in parallel, and synthesize results
- **Storage Efficient Indexing (SEI)** Remove highly unlikely record labels from memory. Proper weights for calculations maintained through summary statistics  $\{H_p\}$  and  $\{H_{p_i}\}$

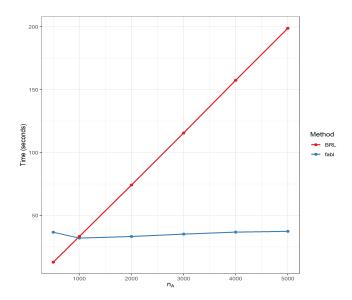
#### Simulation Results 1



#### Simulation Results 2



## Simulation Results 3



#### **Extentions and Directions**

- Linkage in the face of duplicates within datasets
- Models that allow reliability of information to differ by subgroup in the data
- Linkage over blocked data (allows for much larger linkage tasks)

## Questions?

## Additional Slides

## El Salvador

# Distributed computation

# Storage Efficient Indexing