

Record Linkage: Theory and Practice

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U.S. Census Bureau

U S C E N S U S B U R E A U

Introduction

Definition

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Introduction

- Definition
- Terminology

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- Terminology
- Uses

Introduction

- Definition
- Terminology
- Uses
- Context

Definition

- A procedure to find pairs of records in two files that represent the same entity

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- A procedure to find pairs of records in two files that represent the same entity
- When both files are the same file, the procedure is to find duplicate records

Terminology

- Matched records: both records represent the same entity in truth

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- Matched records: both records represent the same entity in truth
- Linked records: Both records are identified by record linkage procedure as probably representing the same entity

Uses

- Updating and deduplicating a survey frame

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- Merging two files for microdata analysis

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- Merging two files for microdata analysis
- Determine confidentiality of microdata

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- Merging two files for microdata analysis
- Determine confidentiality of microdata
- Measure a population by capture-recapture

Capture-Recapture

- Let A, B be independent random samples of sample space S

$$\begin{aligned}x_{11} &= |A \cap B| & x_{10} &= |A \setminus B| \\x_{01} &= |B \setminus A| & x_{00} &= |S \setminus (A \cup B)|\end{aligned}$$

Capture-Recapture

- Let A, B be independent random samples of sample space S

$$\begin{aligned}x_{11} &= |A \cap B| & x_{10} &= |A \setminus B| \\x_{01} &= |B \setminus A| & x_{00} &= |S \setminus (A \cup B)|\end{aligned}$$

- Then

$$\hat{x}_{00} = E[x_{00}] = \frac{x_{1+}x_{+1}}{x_{11}}$$

Capture-Recapture, Cont.

- Take two independent surveys of a region and estimate the number of people missed.

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- Note accuracy of estimate depends on accuracy of x_{11} , as determined by record linkage

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- Y.M.M. Bishop, S.E. Fienberg, P.W. Holland, *Discrete Multivariate Analysis, Theory and Practice*, Chapter 6. MIT Press, 1975

Record Linkage Basics

Context

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Record Linkage Basics

- Context
- Deterministic Record Linkage

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- Probabilistic Record Linkage

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- Probabilistic Record Linkage
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- Files have records of fixed length with fields of fixed length and position (or in a database with retrievable individual fields)

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- Not a search algorithm

Deterministic Record Linkage

- Records are linked when

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- Records are linked when
 - They agree exactly on all matching fields

Deterministic Record Linkage

- Records are linked when
 - They agree exactly on all matching fields
 - Or on predetermined portion of fields

Probabilistic Record Linkage

- Assign a probabilistic weighting to record pairs

Probabilistic Record Linkage

- Assign a probabilistic weighting to record pairs
- Accepts record pairs with sufficiently high weights as linked pairs

Not Statistical Matching

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Not Statistical Matching

- Statistical matching: Bring together pairs of records with statistically similar characteristics, not necessarily representing the same entity
- Usually for two files that represent different samples of a population
- Older practice than exact matching (deterministic or probabilistic)

Need for Automated Record Linkage

Clerical matching is:

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Need for Automated Record Linkage

Clerical matching is:

- expensive

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Clerical matching is:

- expensive

- slow

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	Clerical	1988	1990
Computer match proportion	0%	70%	75%
# clerks	3000	600	200
#months	6	1.5	1.5
False match rate	5%	0.5%	0.2%

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Rec. Link. Theory: Fellegi & Sunter

■ Basic Definitions and Notation

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- Fundamental Theorem

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U.S. CENSUS BUREAU ■ Conditional Independence Assumption

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- Sets of entities A, B

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Agreement Patterns

- Comparison space

$$\alpha(A) \times \beta(B) \rightarrow \Gamma$$

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- Each component of comparison vector can take on finitely many values, typically two

$$\gamma = (\gamma_1, \gamma_2, \dots, \gamma_n)$$

$$\gamma_i \in \{0, 1\}$$

Example Comparison Space

- Consider 3 binary comparisons

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 - γ_1 pair agrees on last name

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- Consider 3 binary comparisons
 - γ_1 pair agrees on last name
 - γ_2 pair agrees on first name
 - γ_3 pair agrees on street name
- Sample agreement pattern

$$\gamma = (1, 0, 1)$$

Conditional Probabilities

- Probability that a record pair has agreement pattern γ , given that it is a match/nonmatch

$$\Pr(\gamma|M)$$

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- Conditioned on the unobservable truth

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Linkage Rule

Designate a record pair's status based on its agreement pattern

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 Link

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$$L : \Gamma \rightarrow \{L, N, C\}$$

Error Rates

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- False nonmatch rate—probability that a designated nonlink is a match

$$\lambda = \Pr(N|M)$$

Error Rates, Cont.

If all pairs of records are designated link or nonlink

Error Rates, Cont.

If all pairs of records are designated link or nonlink

	Match	Nonmatch
Link	$1 - \lambda$	$\mu = \Pr(L U)$
Nonlink	$\lambda = \Pr(N M)$	$1 - \mu$

Clerical Region

- The set C of record pairs which are designated neither probable link nor probable nonlink by the linkage rule

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- The match status of these pairs is left to clerical review

Fundamental Theorem

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- Order the comparison vectors $\{\gamma^j\}$ by their agreement ratios $R(\gamma^j)$

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- Order the comparison vectors $\{\gamma^j\}$ by their agreement ratios $R(\gamma^j)$
- Choose upper T_μ and lower T_λ cutoff values for $R(\gamma)$

Fundamental Theorem, Cont.

Linkage rule:

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Fundamental Theorem, Cont.

Linkage rule:

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Linkage rule:

- Pairs with $R(\gamma^j) \geq T_\mu$ are designated links
- Pairs with $R(\gamma^j) \leq T_\lambda$ are designated nonlinks
- Pairs with $T_\lambda < R(\gamma^j) < T_\mu$ are in the clerical region

Fundamental Theorem, Cont.

The error rates for this linkage rule are

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$$\mu = \sum_{R(\gamma^j) \geq T_\mu} \Pr(\gamma^j | U)$$

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$$\mu = \sum_{R(\gamma^j) \geq T_\mu} \Pr(\gamma^j | U)$$

$$\lambda = \sum_{R(\gamma^j) \leq T_\lambda} \Pr(\gamma^j | M)$$

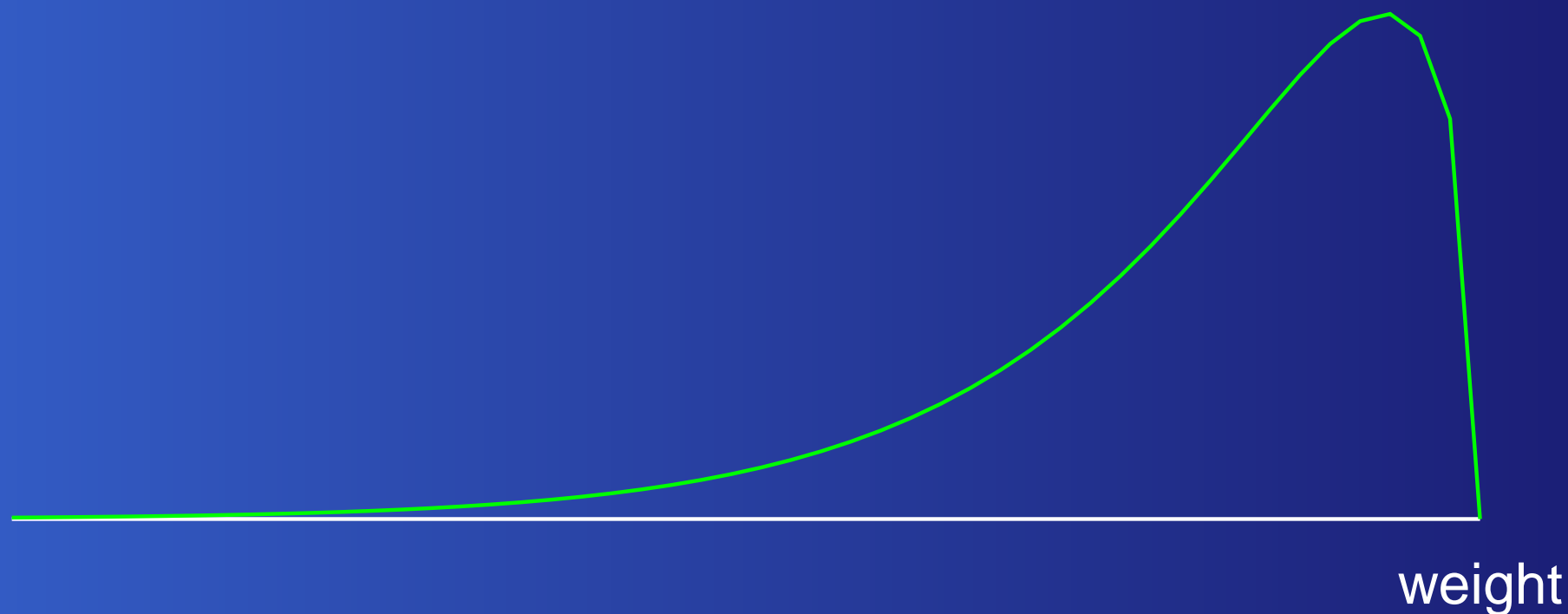
Fundamental Theorem, Cont.

- Theorem: For these error rates μ, λ , this is the optimal linkage rule, in the sense of producing the minimum size critical region

Fundamental Theorem, Cont.

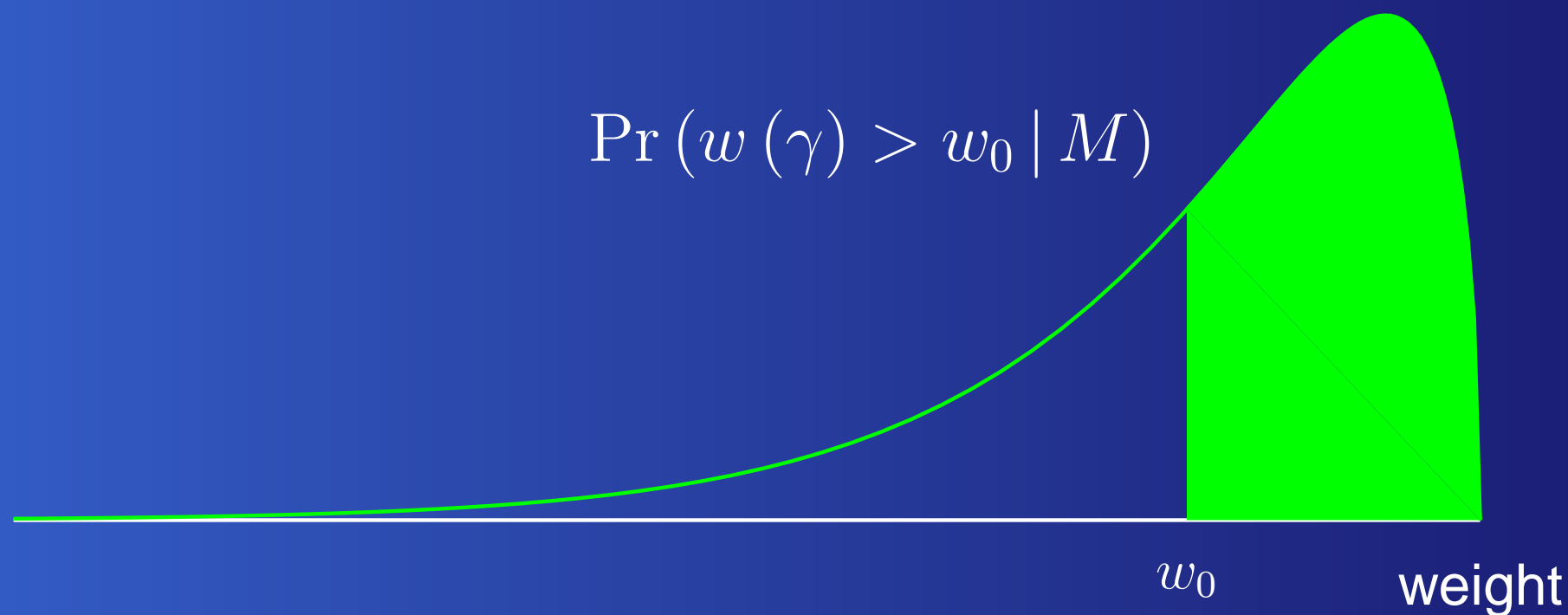
- Theorem: For these error rates μ, λ , this is the optimal linkage rule, in the sense of producing the minimum size critical region
- In other words, for a given error bound tolerance, this rule make as many linkage decisions as possible

Weight Distribution for Matches

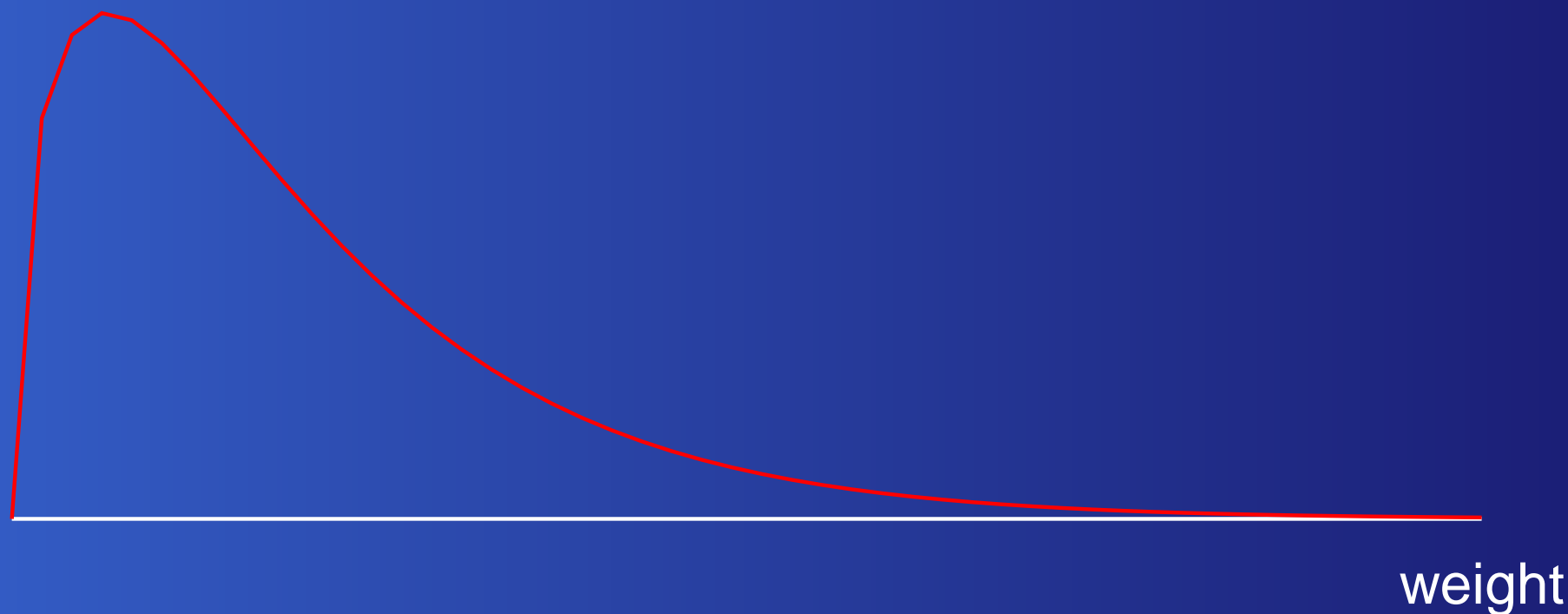


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Weight Distribution for Matches

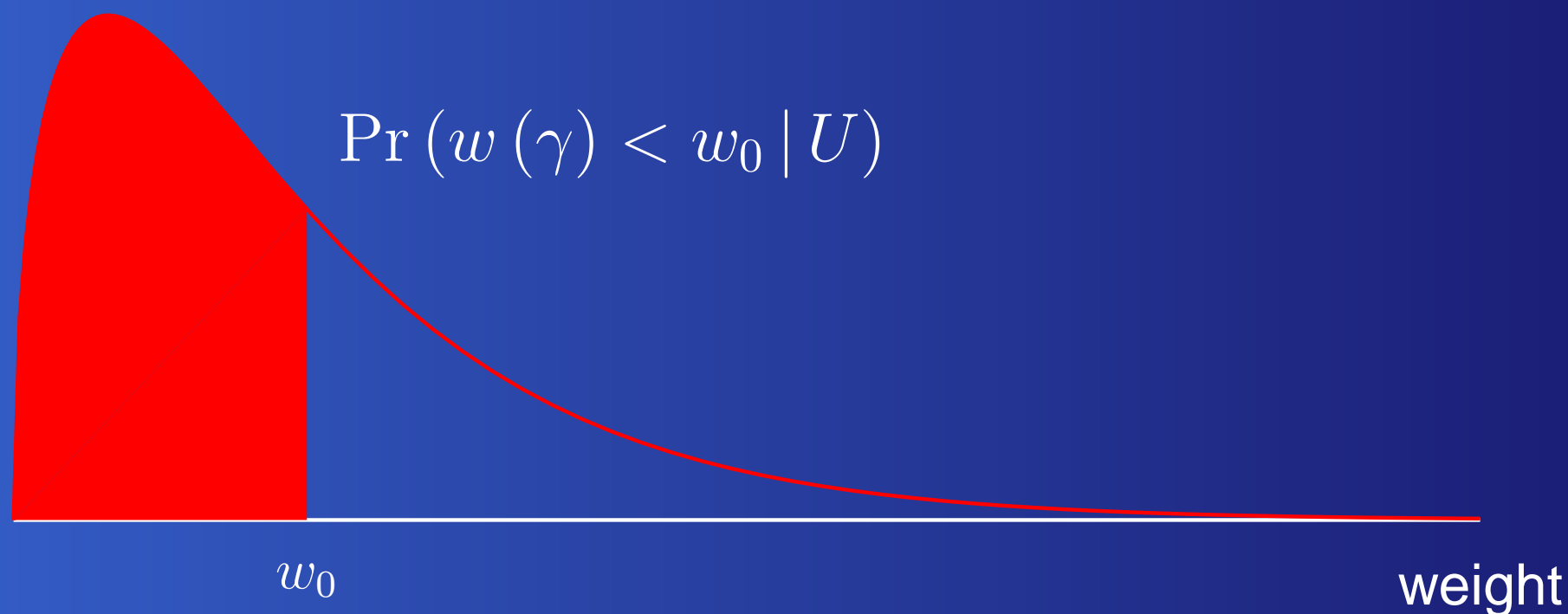


Weight Distribution for Non-Matches

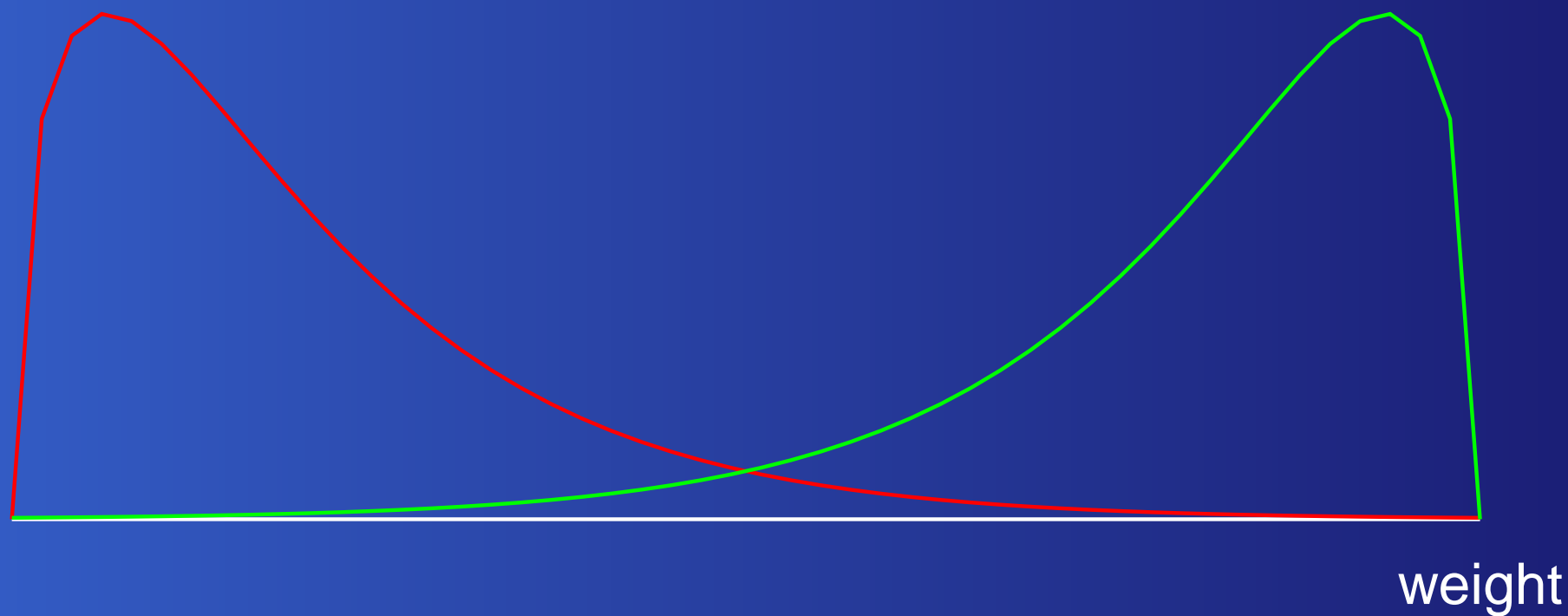


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Weight Distribution for Non-Matches

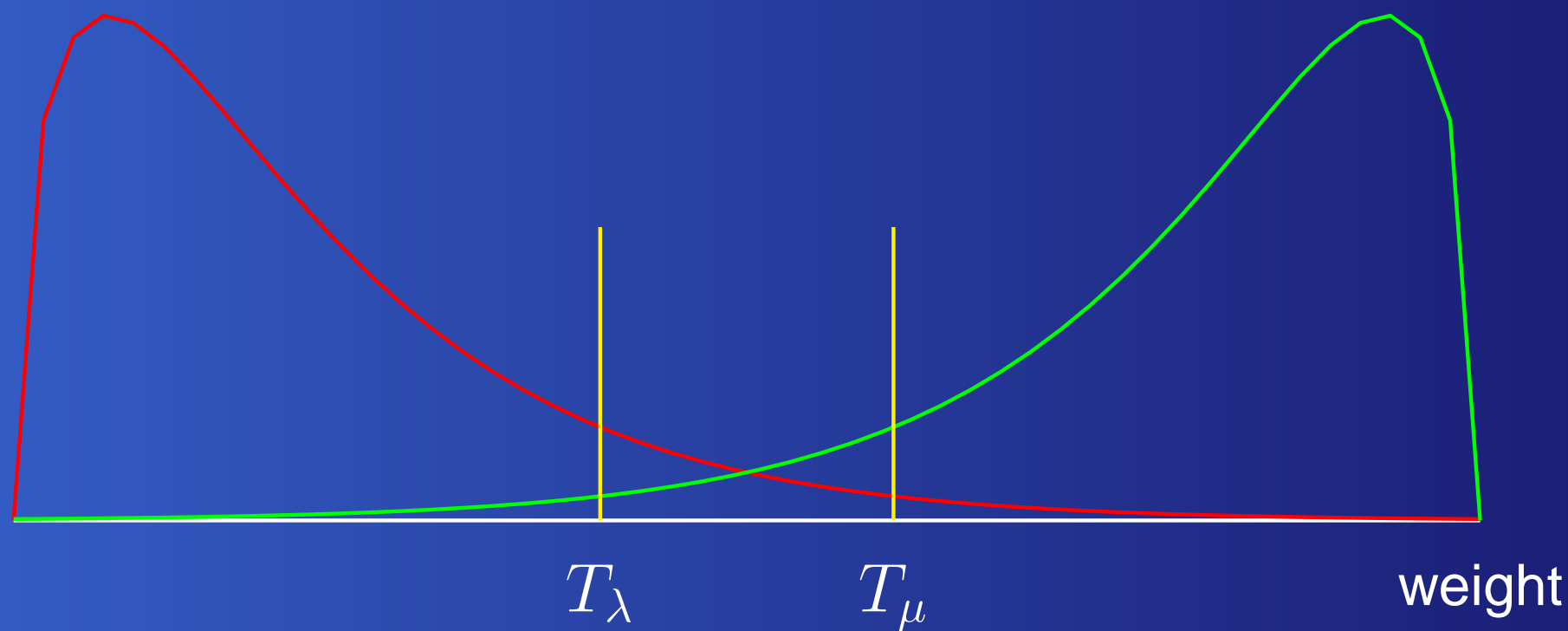


Idealized Distributions



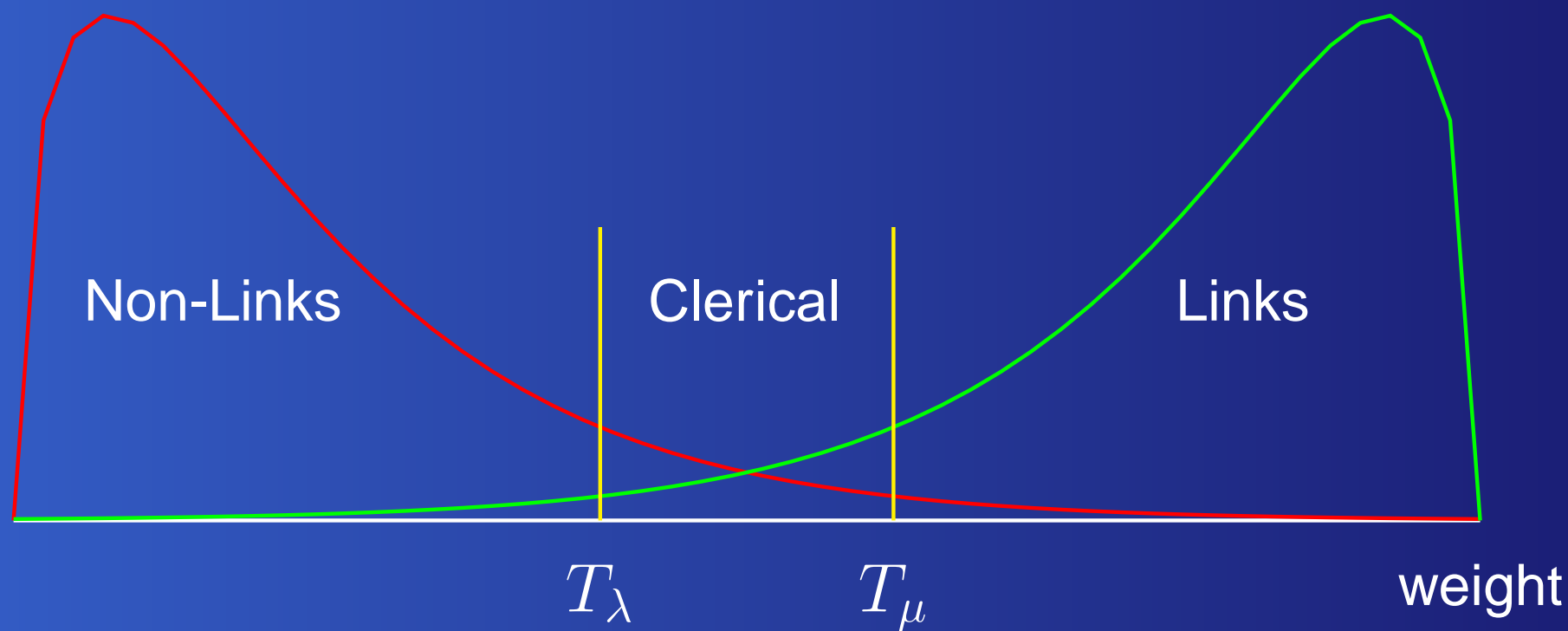
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Idealized Distributions



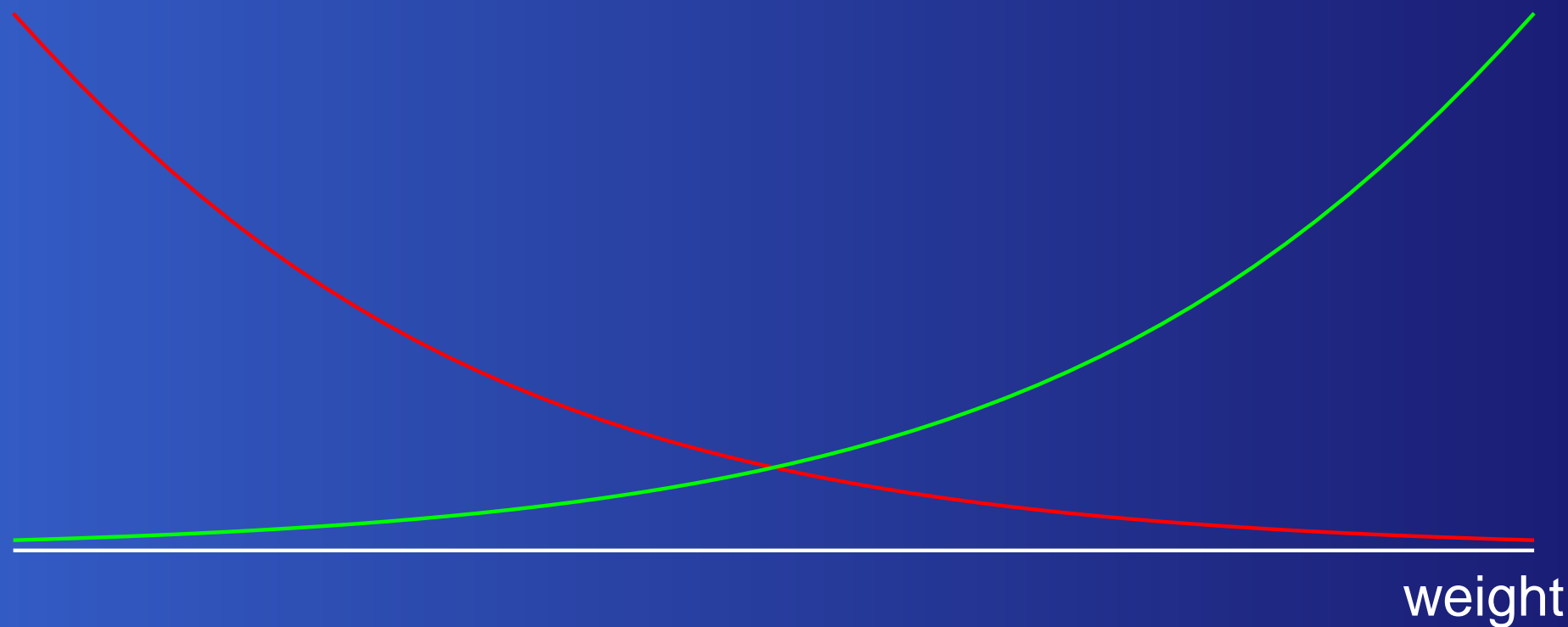
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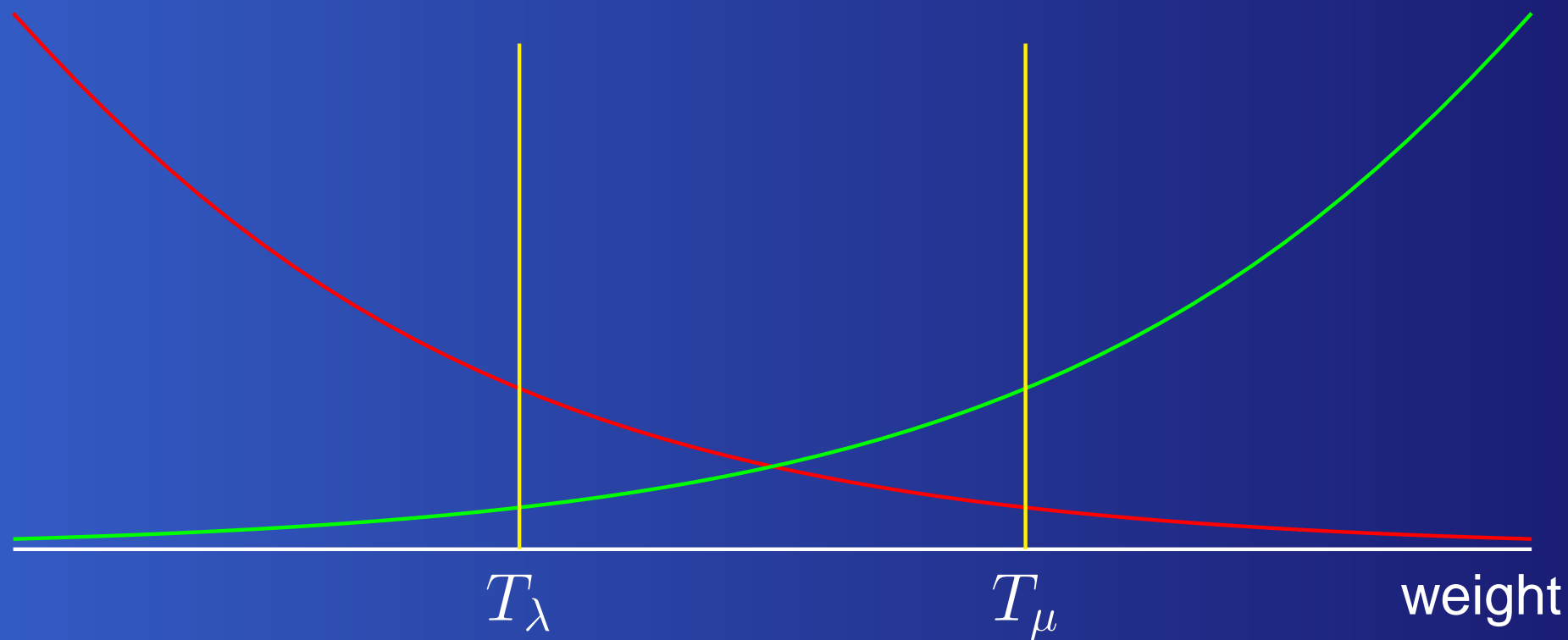
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Error Rates, Clerical Review Region



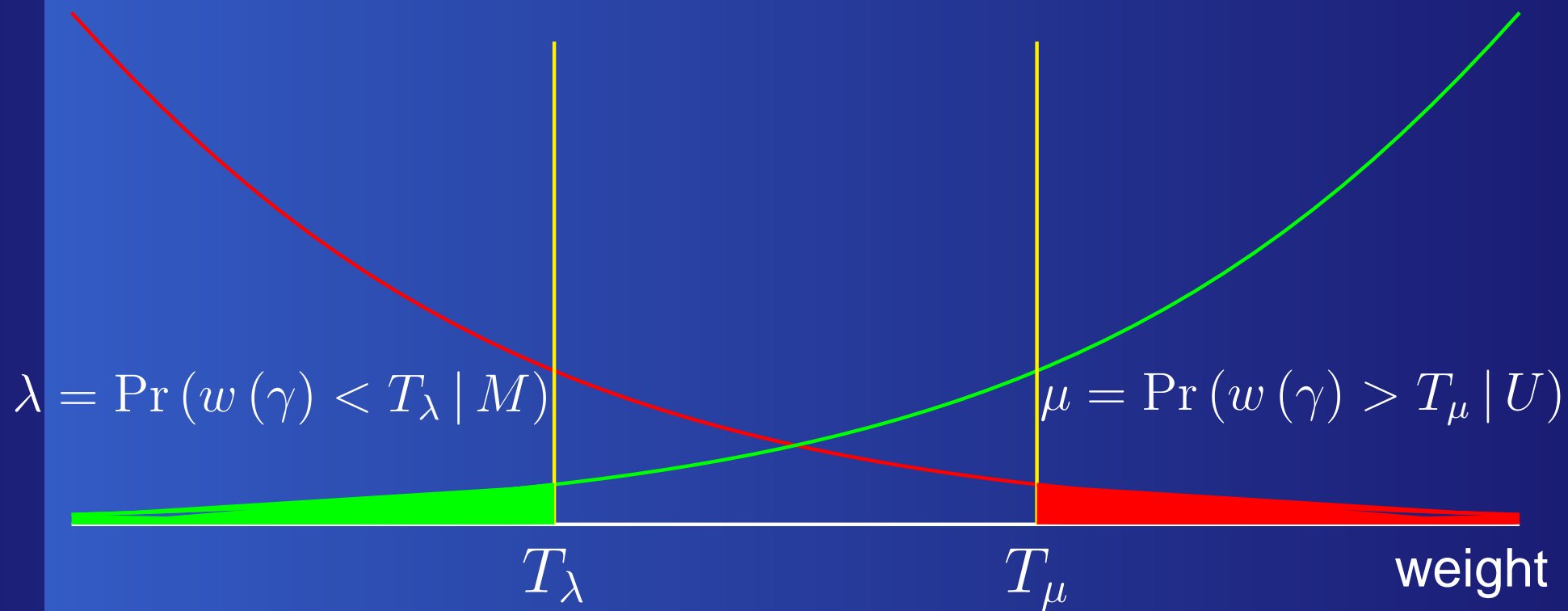
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Error Rates, Clerical Review Region



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Conditional Independence Assumption

- To facilitate computation of conditional probabilities, Fellegi & Sunter assume conditional independence of comparison vector components

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- To facilitate computation of conditional probabilities, Fellegi & Sunter assume conditional independence of comparison vector components
- For $\gamma = (\gamma_1, \gamma_2, \dots, \gamma_n)$, assume

$$\Pr(\gamma|M) = \prod_{i=1}^n \Pr(\gamma_i|M)$$

$$\Pr(\gamma|U) = \prod_{i=1}^n \Pr(\gamma_i|U)$$

Cond. Indep. Assumption, Cont.

- The factors $\Pr(\gamma_i|M)$, $\Pr(\gamma_i|U)$ are called *marginal probabilities*

Cond. Indep. Assumption, Cont.

- The factors $\Pr(\gamma_i|M)$, $\Pr(\gamma_i|U)$ are called *marginal probabilities*

- The ratio

$$\frac{\Pr(\gamma_i|M)}{\Pr(\gamma_i|U)}$$

determines the *distinguishing power* of the comparison γ_i

Cond. Indep. Assumption, Cont.

Under conditional independence assumption, it is convenient to compute the *weight* of the comparison vector

Cond. Indep. Assumption, Cont.

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$$\begin{aligned}w(\gamma) &= \log R(\gamma) \\&= \sum_{i=1}^n \frac{\log \Pr(\gamma_i | M)}{\log \Pr(\gamma_i | U)} \\&= \sum_{i=1}^n w(\gamma_i)\end{aligned}$$

Cond. Indep. Assumption, Cont.

- Motivation: Reduce the number of parameters

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Cond. Indep. Assumption, Cont.

- Motivation: Reduce the number of parameters
- For n binary comparisons and two conditional classes M, U , there are 2^{n+1} parameters
 - 2^n comparison vectors
 - 2 conditional probabilities for each vector
- Under conditional independence assumption, there are $2n$ parameters
- Rationale: Given M , errors producing disagreement should be random

Cond. Indep. Assumption, Cont.

- Often computable in closed form

Cond. Indep. Assumption, Cont.

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- Can produce good decision rules even if model inaccurate

Cond. Indep. Assumption, Cont.

- Often computable in closed form
- Can produce good decision rules even if model inaccurate
- Referred to as *naive Bayes* in machine learning

Conditional Independence Example

■ Suppose

$$\Pr(\gamma_1 = 1|M) = 0.9$$

$$\Pr(\gamma_2 = 1|M) = 0.8$$

$$\Pr(\gamma_3 = 1|M) = 0.7$$

Conditional Independence Example

■ Suppose

$$\Pr(\gamma_1 = 1|M) = 0.9$$

$$\Pr(\gamma_2 = 1|M) = 0.8$$

$$\Pr(\gamma_3 = 1|M) = 0.7$$

■ Then for $\gamma = (1, 0, 1)$,

$$\Pr(\gamma|M) = 0.9 * 0.2 * 0.7 = 0.126$$

Conditional Independence Example

■ Suppose

$$\Pr(\gamma_1|M) = 0.8 \quad \Pr(\gamma_1|U) = 0.1$$

$$\Pr(\gamma_2|M) = 0.9 \quad \Pr(\gamma_2|U) = 0.3$$

Conditional Independence Example

■ Suppose

$$\Pr(\gamma_1|M) = 0.8 \quad \Pr(\gamma_1|U) = 0.1$$

$$\Pr(\gamma_2|M) = 0.9 \quad \Pr(\gamma_2|U) = 0.3$$

■ Then

$$\frac{\Pr(\gamma_1|M)}{\Pr(\gamma_1|U)} = 8.0$$

$$\frac{\Pr(\gamma_2|M)}{\Pr(\gamma_2|U)} = 3.0$$

Fellegi-Sunter Summary

- Choose conditional probability parameters

Fellegi-Sunter Summary

- Choose conditional probability parameters
- Conduct field comparisons on record pairs

Fellegi-Sunter Summary

- Choose conditional probability parameters
- Conduct field comparisons on record pairs
- Classify record pairs based on weight of comparison vector

Record Linkage Methodology

- Parameter estimation

Record Linkage Methodology

- Parameter estimation
 - EM Algorithm

Record Linkage Methodology

- Parameter estimation
 - EM Algorithm
- Blocking

Choosing Parameters

■ Informal

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- Informal
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Choosing Parameters

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- Other Methods

Informal Methods

 Guess

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Informal Methods

■ Guess

$$0 < \Pr(\gamma|U) < \Pr(\gamma|M) < 1$$

Informal Methods

- Guess

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- Perform matching with current parameters

Informal Methods

■ Guess

$$0 < \Pr(\gamma|U) < \Pr(\gamma|M) < 1$$

■ Approximate

$$\Pr(\gamma|U) \approx \Pr(\gamma|S)$$

■ Iterate

- Perform matching with current parameters
- Review results

Informal Methods

■ Guess

$$0 < \Pr(\gamma|U) < \Pr(\gamma|M) < 1$$

■ Approximate

$$\Pr(\gamma|U) \approx \Pr(\gamma|S)$$

■ Iterate

- Perform matching with current parameters
- Review results
- Adjust parameters based on observation

EM Algorithm

- Dempster, Laird, Rubin. “Maximum likelihood from incomplete data via the EM algorithm”. *Journal of the Royal Statistical Society. Series B.* **39.** pp. 1–39. 1977.

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- McLachlan, Krishnan. *The EM Algorithm and Extensions*. Wiley-Interscience. 2nd Ed. 2007.

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- Mixture model

Likelihood Function



$$\begin{aligned} L &= \prod_{(a,b) \in S} \Pr(\gamma(a, b)) \\ &= \prod_j \left(\Pr(\gamma^j | M) \Pr(M) + \Pr(\gamma^j | U) \Pr(U) \right)^{n_j} \end{aligned}$$

Likelihood Function



$$\begin{aligned} L &= \prod_{(a,b) \in S} \text{Pr}(\gamma(a,b)) \\ &= \prod_j \left(\text{Pr}(\gamma^j | M) \text{Pr}(M) + \text{Pr}(\gamma^j | U) \text{Pr}(U) \right)^{n_j} \end{aligned}$$



$$n_j = \left| \{ (a,b) \in S \mid \gamma(a,b) = \gamma^j \} \right|$$

Complete-data Likelihood Function

■ Consider

$$\chi_j = \begin{cases} 1 & \text{if } (a, b)^j \in M \\ 0 & \text{if } (a, b)^j \in U \end{cases}$$

$$X_j = \sum_{\gamma(a,b)=\gamma^j} \chi_j(a, b)$$

Complete-data Likelihood Function

■ Consider

$$\chi_j = \begin{cases} 1 & \text{if } (a, b)^j \in M \\ 0 & \text{if } (a, b)^j \in U \end{cases}$$

$$X_j = \sum_{\gamma(a,b)=\gamma^j} \chi_j(a, b)$$

■ Then

$$L = \prod_j \left((\Pr(\gamma^j | M) \Pr(M))^{\bar{X}_j} (\Pr(\gamma^j | U) \Pr(U))^{1 - \bar{X}_j} \right)^{n_j}$$

Expectation Step

- Given current estimates of conditional probabilities and $\Pr(M)$, $\Pr(U)$, compute

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$$\begin{aligned} E(\overline{X}^j) &= \Pr(M|\gamma^j) \\ &= \frac{\Pr(\gamma^j|M) \Pr(M)}{\Pr(\gamma^j|M) \Pr(M) + \Pr(\gamma^j|U) \Pr(U)} \\ &= \hat{X}^j \end{aligned}$$

Maximization Step

- Given unobserved data estimates \hat{X}^j , compute probabilities $\Pr(\gamma^j|M)$, $\Pr(\gamma^j|U)$, $\Pr(M)$, $\Pr(U)$ maximizing

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$$\log L =$$

$$\sum_j n_j \left(\hat{X}^j (\log \Pr(\gamma^j|M) + \log \Pr(M)) + (1 - \hat{X}^j) (\log \Pr(\gamma^j|U) + \log \Pr(U)) \right)$$

Max Step, Cont.

- Under conditional independence

Max Step, Cont.

- Under conditional independence

$$\begin{aligned} \log L = & \sum_j n_j \left(\sum_i \hat{X}^j \left(\log \Pr \left(\gamma_i^j | M \right) + \log \Pr (M) \right) \right. \\ & \left. + \left(1 - \hat{X}^j \right) \left(\sum_i \log \Pr \left(\gamma_i^j | U \right) + \log \Pr (U) \right) \right) \end{aligned}$$

Max Step, Cont.

For

$$n = \sum_j n_j$$

estimate

$$\Pr(M) = \frac{1}{n} \sum_j n_j \bar{X}^j$$

Max Step, Cont.

■ Let

$$k_i^j = \begin{cases} 1 & \text{if } \gamma_i^j = 1 \\ 0 & \text{if } \gamma_i^j = 0 \end{cases}$$

Max Step, Cont.

■ Let

$$k_i^j = \begin{cases} 1 & \text{if } \gamma_i^j = 1 \\ 0 & \text{if } \gamma_i^j = 0 \end{cases}$$

■ and estimate

$$\Pr(\gamma_i | M) = \frac{1}{n} \sum_j n_j \bar{X}^j k_i^j$$

EM Algorithm

1. Initialize with probability values

EM Algorithm

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2. Iterate

EM Algorithm

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 - (a) Expectation Step

EM Algorithm

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 - (b) Maximization Step

EM Algorithm

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2. Iterate
 - (a) Expectation Step
 - (b) Maximization Step
3. Until convergence of likelihood function

EM Algorithm Remarks

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- Each EM iteration increases likelihood, so algorithm converges to a (local) maximum
- For this conditional independence model, convergence is efficient and generally insensitive to initial data
- For latent class to be numerically detected, it must be represented by about 5% of the total record pair data
- Check: Do $\Pr(M)$, $\Pr(U)$ seem reasonable?

EM Remarks, Cont.

- If $\text{Pr}(M)$, $\text{Pr}(U)$ are off, everything is off

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- If $\text{Pr}(M)$, $\text{Pr}(U)$ are off, everything is off
- We can extend problem to comparisons taking on more than 2 values
 - Creates more pattern types and probability parameters
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 - Increases number of parameters to be estimated

Blocking

- If set A contains m records and set B contains n records then $A \times B$ contains mn record pairs

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- Generally repeat record linkage procedure for several different blocking criteria

U S C E N S U S B U R E A U

Blocking Criteria

- Geographic codes

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- Postal or phone codes

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Blocking Criteria

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- Combinations

Record Linkage Refinements

- String comparator

Record Linkage Refinements

- String comparator
- Third latent class

Record Linkage Refinements

- String comparator
- Third latent class
- Third comparison value

Record Linkage Refinements

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- One-to-one matching

String Comparator

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String Comparator

- For some comparisons (e.g. categorical variables), it is sufficient to assign agree/disagree
- For string variables (e.g. first names, last names, street names) this is probably too restrictive
- A string comparator allows us to assign comparison values between full agreement and full disagreement

String Comparator Context

- Binary comparison $\gamma \in \{0, 1\}$

String Comparator Context

- Binary comparison $\gamma \in \{0, 1\}$
- Weight assignment

$$a_w = \log \frac{\Pr(\gamma = 1|M)}{\Pr(\gamma = 1|U)}$$

$$d_w = \log \frac{\Pr(\gamma = 0|M)}{\Pr(\gamma = 0|U)}$$

$$d_w < 0 < a_w$$

String Comparator Context, Cont.

- For alphabet Σ , our string comparator is a *similarity function*

$$\gamma : \Sigma^* \times \Sigma^* \rightarrow [0, 1]$$

$$\gamma(\alpha, \beta) = 1 \text{ if } \alpha = \beta$$

String Comparator Context, Cont.

- For alphabet Σ , our string comparator is a *similarity function*

$$\gamma : \Sigma^* \times \Sigma^* \rightarrow [0, 1]$$

$$\gamma(\alpha, \beta) = 1 \text{ if } \alpha = \beta$$

- Weight assignment function w is an increasing interpolation function

$$w : [0, 1] \rightarrow [d_w, a_w]$$

$$w(1) = a_w$$

Some String Comparator Types

- Bigram, n -gram

Some String Comparator Types

- Bigram, n -gram
- Jaro-Winkler

Some String Comparator Types

- Bigram, n -gram
- Jaro-Winkler
- Edit distance

Bigrams

- Decompose string into a set of 2-character (contiguous) substrings

alphabet $\rightarrow \{al, lp, ph, ha, ab, be, et\}$

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alphabet $\rightarrow \{al, lp, ph, ha, ab, be, et\}$

- For alphabet of $s = |\Sigma|$ characters, record bigram counts in a vector of dimension s^2

Bigrams, Cont.

- Two strings can be compared by computing the “angle” between their bigram vectors a, b

$$\cos \theta = \frac{a \cdot b}{|a| |b|}$$

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- Obvious generalization to n -grams
- Vector for n -gram is in s^n dimensional space

Bigrams, Cont.

- Computation algorithm is fast (linear)

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- Don't work very well for record linkage

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$$abcba \approx bcbab$$

Bigrams, Cont.

- Computation algorithm is fast (linear)
- Don't work very well for record linkage
 - Ignores order of bigram occurrence

$$abcba \approx bcbab$$

- Works better for small alphabet, long strings than *vice versa*

Jaro-Winkler Comparator

- In the following, let $\alpha = (a_1, a_2, \dots, a_m)$, $\beta = (b_1, b_2, \dots, b_n)$ be strings of lengths m, n respectively with $m \leq n$

Jaro-Winkler Comparator

- In the following, let $\alpha = (a_1, a_2, \dots, a_m)$, $\beta = (b_1, b_2, \dots, b_n)$ be strings of lengths m, n respectively with $m \leq n$
- Comparator value depends on number of common characters and character “transpositions”

Jaro-Winkler Comparator, Cont.

- Strings α, β have common characters a_i, b_j iff

$$\begin{aligned} a_i &= b_j \\ |i - j| &< \left\lfloor \frac{n}{2} \right\rfloor \end{aligned}$$

Jaro-Winkler Comparator, Cont.

- Strings α, β have common characters a_i, b_j iff

$$\begin{aligned} a_i &= b_j \\ |i - j| &< \left\lfloor \frac{n}{2} \right\rfloor \end{aligned}$$

- The number of transpositions is computed as the greatest integer of half of the number of out-of-order common character pairs

Jaro-Winkler Comparator, Cont.

- For string pair with c common characters and t transpositions, basis similarity score is

$$x = \frac{1}{3} \left(\frac{c}{m} + \frac{c}{n} + \frac{c - t}{c} \right)$$

Jaro-Winkler Example

- Consider the strings (b,a,r,n,e,s) and (a,n,d,e,r,s,o,n)

Jaro-Winkler Example

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- Search range d

$$\begin{aligned}n &= 8 \\d &= \left\lfloor \frac{8}{2} \right\rfloor - 1 = 3\end{aligned}$$

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- Consider the strings (b,a,r,n,e,s) and (a,n,d,e,r,s,o,n)
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$$\begin{aligned}n &= 8 \\d &= \left\lfloor \frac{8}{2} \right\rfloor - 1 = 3\end{aligned}$$

- Common characters

(a, r, n, e, s)

(a, n, e, r, s)

Jaro-Winkler Example, Cont.

- Five common characters with 3 out of order, so $c = 5, t = 1$

Jaro-Winkler Example, Cont.

- Five common characters with 3 out of order, so $c = 5, t = 1$
- Score

$$x = \frac{1}{3} \left(\frac{5}{6} + \frac{5}{8} + \frac{4}{5} \right) = \frac{271}{360} \doteq 0.75280$$

Jaro-Winkler Variations

- Similar characters

Jaro-Winkler Variations

- Similar characters
- Prefix adjustment

Jaro-Winkler Variations

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Similar Characters

- Attempt to compensate for common misspellings or typos

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- List of 36 pairs of characters deemed similar (e.g. most vowel pairs)
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- Each similar pair is scored as 0.3 of a common pair

Similar Characters, Cont.

- Revised character count

$$c_s = c + 0.3s$$

Similar Characters, Cont.

- Revised character count

$$c_s = c + 0.3s$$

- Adjusted comparator score

$$x_s = \frac{1}{3} \left(\frac{c_s}{m} + \frac{c_s}{n} + \frac{c - t}{c} \right)$$

Similar Characters, Cont.

- For example. *abc* and *ebc* have 2 common characters and the remaining pair (*a,e*) are similar, so

$$\begin{aligned}x_s &= \frac{1}{3} \left(\frac{2}{3} + \frac{2}{3} + 1 \right) + \frac{1}{3} \left(\frac{0.3}{3} + \frac{0.3}{3} \right) \\&= \frac{7}{9} + \frac{1}{15} \\&= \frac{38}{45}\end{aligned}$$

Common Prefix

- Spelling mistakes tend to occur later in the string (Winkler)

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Common Prefix

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- Check for common prefix of up to 4 characters
- If length of common prefix is p , adjust score x by

$$x_p = x + \frac{p(1 - x)}{10}$$

Long String Adjustment

- Adjust score for longer strings with several common characters beyond common prefix

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 3. $c - p \geq \frac{m-p}{2}$

Long String Adjustment, Cont.

■ That is,

Long String Adjustment, Cont.

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1. Both strings are at least 5 characters long

Long String Adjustment, Cont.

■ That is,

1. Both strings are at least 5 characters long
2. There are at least two common characters besides the agreeing prefix characters

Long String Adjustment, Cont.

■ That is,

1. Both strings are at least 5 characters long
2. There are at least two common characters besides the agreeing prefix characters
3. We want the strings outside the common prefixes to be fairly rich in common characters, so that the remaining common characters are at least half of the remaining common characters of the shorter string

Long String Adjustment, Cont.

- If conditions met, then adjust score by

$$x_l = x + (1 - x) \frac{c - (p + 1)}{m + n - 2(p - 1)}$$

Long String Adjustment, Cont.

- In *barnes, anderson* example, conditions are met, so the adjusted score is

$$\begin{aligned}x_l &= \frac{271}{360} + \left(1 - \frac{271}{360}\right) \frac{5 - 1}{6 + 8 + 2} \\&= \frac{391}{480} \\&\doteq 0.8146\end{aligned}$$

Jaro-Winkler Comparator

- Slower algorithm (quadratic)

Jaro-Winkler Comparator

- Slower algorithm (quadratic)
- Performs very well in tests

Edit Distance String Comparators

- The minimum number of edits required to convert string α to string β , lengths $m \leq n$

Edit Distance String Comparators

- The minimum number of edits required to convert string α to string β , lengths $m \leq n$
 - Insert

Edit Distance String Comparators

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Edit Distance String Comparators

- The minimum number of edits required to convert string α to string β , lengths $m \leq n$
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 - Delete
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- Dynamic programming algorithm, quadratic complexity $O(mn)$

Edit Distance Algorithm

- For α_i prefix of α of length i , β_j prefix of β of length j

Edit Distance Algorithm

- For α_i prefix of α of length i , β_j prefix of β of length j
- Initialize

$$e(\alpha_i, \varepsilon) = i$$

$$e(\varepsilon, \beta_j) = j$$

$$e(\varepsilon, \varepsilon) = 0$$

Edit Distance Algorithm, Cont.

■ Compute

$$e(\alpha_i, \beta_j) = \min \begin{cases} e(\alpha_{i-1}, \beta_j) + 1 \\ e(\alpha_i, \beta_{j-1}) + 1 \\ \begin{cases} e(\alpha_{i-1}, \beta_{j-1}) & \text{if } a_i = b_j \\ e(\alpha_{i-1}, \beta_{j-1}) + 1 & \text{if } a_i \neq b_j \end{cases} \end{cases}$$

Edit Distance Algorithm, Cont.

■ Compute

$$e(\alpha_i, \beta_j) = \min \begin{cases} e(\alpha_{i-1}, \beta_j) + 1 \\ e(\alpha_i, \beta_{j-1}) + 1 \\ \begin{cases} e(\alpha_{i-1}, \beta_{j-1}) & \text{if } a_i = b_j \\ e(\alpha_{i-1}, \beta_{j-1}) + 1 & \text{if } a_i \neq b_j \end{cases} \end{cases}$$

■ Distance

$$e = e(\alpha, \beta) = e(\alpha_m, \beta_n)$$

Edit Distance Similarity Function

- Edit distance is a metric

Edit Distance Similarity Function

- Edit distance is a metric
- Similarity function

$$x_e = 1 - \frac{e}{n}$$

Edit Distance Example

- For example, for *barnes*, *anderson*, have possible minimal edit path

$(b, \varepsilon) a (r, n) (n, d) e (\varepsilon, r) s (\varepsilon, o) (\varepsilon, n)$

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$(b, \varepsilon) a (r, n) (n, d) e (\varepsilon, r) s (\varepsilon, o) (\varepsilon, n)$

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$$x_e = 1 - \frac{6}{8} = \frac{1}{4}$$

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- Note order of characters very important

Longest Common Subsequence

- Length of longest common subsequence (lcs)

Longest Common Subsequence

- Length of longest common subsequence (*lcs*)
- Similar dynamic programming algorithm, without substitutions

$$e(\alpha_i, \beta_j) = \min \begin{cases} e(\alpha_{i-1}, \beta_j) + 1 \\ e(\alpha_i, \beta_{j-1}) + 1 \\ e(\alpha_{i-1}, \beta_{j-1}) \quad \text{if } a_i = b_j \end{cases}$$

LCS Similarity Function

- Similarity function

$$x_c = \frac{l}{m}$$

LCS Similarity Function

- Similarity function

$$x_c = \frac{l}{m}$$

- Example $lcs = (a, n, e, s)$, similarity score

$$x_c = \frac{4}{6} = \frac{2}{3}$$

Combination Similarity Function

- Compute both edit distance and lcs

Combination Similarity Function

- Compute both edit distance and lcs
- Combined score

$$x_{ec} = \frac{1}{2} \left(\left(1 - \frac{e}{n} \right) + \frac{l}{m} \right)$$

Combination Similarity Function

- Compute both edit distance and *lcs*
- Combined score

$$x_{ec} = \frac{1}{2} \left(\left(1 - \frac{e}{n} \right) + \frac{l}{m} \right)$$

- Example

$$x_{ec} = \frac{1}{2} \left(\frac{1}{4} + \frac{2}{3} \right) = \frac{11}{24} \doteq 0.4583$$

Evaluating String Comparators

- Yancey, “Evaluating String Comparator Performance for Record Linkage,” 2005, <http://www.census.gov/srd/www/byname.html>

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 - Edit distance

Evaluating String Comparators, Cont.

- Jaro-Winkler, with and without modifications

Evaluating String Comparators, Cont.

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 - Prefix adjustment

Evaluating String Comparators, Cont.

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 - Similar characters

Evaluating String Comparators, Cont.

- Jaro-Winkler, with and without modifications
 - Prefix adjustment
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 - Long suffix adjustment

Evaluating String Comparators, Cont.

- Edit distance

Evaluating String Comparators, Cont.

- Edit distance
 - Edit distance similarity

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- Edit distance
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 - Markov edit distance (J. Wei. “Markov Edit Distance”. *IEEE Transactions on Pattern Analysis and Machine Intelligence*, Vol 26, No. 3, pp. 311–321, 2004)

Evaluating String Comparators, Cont.

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 - Edit distance similarity
 - Markov edit distance (J. Wei. “Markov Edit Distance”. *IEEE Transactions on Pattern Analysis and Machine Intelligence*, Vol 26, No. 3, pp. 311–321, 2004)
 - With and without *lcs*

Evaluating String Comparators, Cont.

- Lots of data

USCENSUSBUREAU

Evaluating String Comparators, Cont.

- Lots of data
- Truth decks from 1990 and 2000 U.S. Census

USCENSUSBUREAU

Evaluating String Comparators, Cont.

- Lots of data
- Truth decks from 1990 and 2000 U.S. Census
- M : All non-identical, non-blank names from matched record pairs

Evaluating String Comparators, Cont.

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- Truth decks from 1990 and 2000 U.S. Census
- M : All non-identical, non-blank names from matched record pairs
- U : All cross pairs of these names

Results of String Comparator Evaluation

- Jaro-Winkler did well

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Results of String Comparator Evaluation

- Adding *lcs* significantly improves edit distance and Markov edit distance

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- Jaro-Winkler (full) comparable to edit distance/*lcs*

Results of String Comparator Evaluation

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- Edit distance always better than Markov edit distance
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Jaro-Winkler Anomaly

- Let α, β be strings of length n with no common characters

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 - $s(\alpha, \alpha\beta) = \frac{5}{6}$

Jaro-Winkler Anomaly

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- For Jaro-Winkler
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 - In $n \geq 4$, with prefix adjustment,
 $s(\alpha, \alpha\beta) = \frac{9}{10}$

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 - $s(\beta, \alpha\beta) = 0$

Jaro-Winkler Anomaly

- Let α, β be strings of length n with no common characters
- For Jaro-Winkler
 - $s(\alpha, \alpha\beta) = \frac{5}{6}$
 - In $n \geq 4$, with prefix adjustment,
 $s(\alpha, \alpha\beta) = \frac{9}{10}$
 - $s(\beta, \alpha\beta) = 0$
- For edit-distance/lcs, $s(\alpha, \alpha\beta) = s(\beta, \alpha\beta) = \frac{3}{4}$

Hybrid Comparator

- Compute both Jaro-Winkler and edit distance/lcs

Hybrid Comparator

- Compute both Jaro-Winkler and edit distance/lcs
- Use larger of Jaro-Winkler and (scaled) edit distance/lcs

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- Use larger of Jaro-Winkler and (scaled) edit distance/lcs
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- Where J-W does significantly worse, hybrid does nearly as well as edit distance/lcs

Hybrid Comparator, Cont.

- Can see some improvement in actual record linkage results

Hybrid Comparator, Cont.

- Can see some improvement in actual record linkage results
- Calculation takes a long time

String Comparator Summary

- String comparator improves record linkage

String Comparator Summary

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- String comparator takes significant amount of record linkage computation time

String Comparator Summary

- String comparator improves record linkage
- String comparator takes significant amount of record linkage computation time
 - For J-W, about 30%

More Than Two Latent Classes

- EM algorithm generalizes to more than 2 classes, M, U

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- Does U have any natural partitions?

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- For Census data
 - U_1 , different people, same household
 - U_2 , different people, different household

More Than Two Latent Classes

- EM algorithm generalizes to more than 2 classes, M, U
- Does U have any natural partitions?
- For Census data
 - U_1 , different people, same household
 - U_2 , different people, different household
- Classes have to be implicit in the matching data

EM for Three Classes

- Use EM to estimate $\Pr(U_1)$, $\Pr(U_2)$, and marginal probabilities $\Pr(\gamma_i|U_1)$, $\Pr(\gamma_i|U_2)$

EM for Three Classes

- Use EM to estimate $\Pr(U_1)$, $\Pr(U_2)$, and marginal probabilities $\Pr(\gamma_i|U_1)$, $\Pr(\gamma_i|U_2)$
- Recombine

$$\Pr(\gamma_i|U) = \frac{\Pr(\gamma_i|U_1) \Pr(U_1) + \Pr(\gamma_i|U_2) \Pr(U_2)}{\Pr(U_1) + \Pr(U_2)}$$

More Than Two Comparison Values

- Can have more than {agree, disagree}

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- For m comparison values, EM algorithm must estimate $2(m - 1)$ parameters
- We have used {agree, disagree, missing} when data is often missing but has distinguishing power when present
 - For example, middle initial

More Than Two Compr. Values, Cont.

- Reasonability check for parameter estimation

$$\log \frac{\Pr(\text{blank}|M)}{\Pr(\text{blank}|U)} \approx 0$$

One-to-one Matching

- If both files have no duplication within them, then it is preferable to have output with each record linked to no more than one record in the other file

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- If both files have no duplication within them, then it is preferable to have output with each record linked to no more than one record in the other file
- All records that are compared with each other are within a block
- Linear assignment algorithm used to find optimal one-to-one matches within a block

Linear Assignment Algorithm

- For agreement weights in block

	B_1	B_2	B_3	\dots	B_n
A_1	w_{11}	w_{12}	w_{13}		w_{1n}
A_2	w_{21}	w_{22}	w_{23}		w_{2n}
A_3	w_{31}	w_{32}	w_{33}		w_{3n}
\vdots					
A_n	w_{n1}	w_{n2}	w_{n3}		w_{nn}

Linear Assignment Algorithm

- Find permutation $\bar{\sigma}$ that maximizes

$$\sum_{i=1}^n w_{i,\sigma(i)}$$

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- Not a greedy algorithm

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Father	40	\leftrightarrow	Mother	39
Mother	39	\leftrightarrow	Daughter	16
Daughter	16	\leftrightarrow	Son	13
Son	13			

Error Rates

False Match Rate

$$\mu = \Pr(L | U) = \Pr(w(\gamma) < T_\mu | U)$$

Error Rates

False Match Rate

$$\mu = \Pr(L | U) = \Pr(w(\gamma) < T_\mu | U)$$

False Non-match Rate

$$\lambda = \Pr(N | M) = \Pr(w(\gamma) > T_\lambda | U)$$

Practical Considerations

- Question: Relative to what sample space?

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 - After 1-1 matching

Practical Considerations

- Question: Relative to what sample space?
 - $A \times B$
 - Pairs in blocking scheme
 - After 1-1 matching
- Each step presumably filters out a lot of low-weight pairs

False Non-Match Rate

- Difficult to determine as well as define

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- May as well try to estimate number of undiscovered matches in $A \times B$

False Non-Match Rate

- Difficult to determine as well as define
- May as well try to estimate number of undiscovered matches in $A \times B$
- Can try capture-recapture using *independent* blocking schemes

False Match Rate

- Bellin-Rubin

False Match Rate

- Bellin-Rubin
- Larsen

False Match Rate

- Bellin-Rubin
- Larsen
- Larsen, Rubin, Winkler

Bellin-Rubin

- Bellin, T.R. and Rubin, D.B. (1995) “A Method for Calibrating False-Match Rates in Record Linkage,” *Journal of the American Statistical Association*, 90, pp.694–707.

Bellin-Rubin

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- Consider sample space without 1-1 matching
- Model as a mixture of 2 normal distributions (Box-Cox)

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- Consider sample space without 1-1 matching
- Model as a mixture of 2 normal distributions (Box-Cox)
- M and U must be well-separated and unimodal

Larsen

- Larsen, M.D. “Hierarchical Bayesian Record Linkage Theory,” Iowa State University, Statistics Department Technical Report

Larsen

- Larsen, M.D. “Hierarchical Bayesian Record Linkage Theory,” Iowa State University, Statistics Department Technical Report
- Estimate error rates with 1-1 matching

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- Estimate error rates with 1-1 matching
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- Metropolis-Hastings procedure

Improved Parameter Estimates

- Recall, if we had correct parameter values (and model), under Fellegi-Sunter, error rates are known

Improved Parameter Estimates

- Recall, if we had correct parameter values (and model), under Fellegi-Sunter, error rates are known
- Improve parameter estimates using training data

Extended Likelihood Function

- For unlabeled sample space S and labeled training data set T , extended likelihood function

$$L = \left(\prod_{(a,b) \in S} \Pr(\gamma(a,b)) \right)^{1-\lambda} \left(\prod_{(a,b) \in T} \Pr(\gamma(a,b)) \right)^{\lambda}$$

for $0 \leq \lambda \leq 1$

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- Estimate using EM

Larsen, Rubin

- Larsen, M.D. and Rubin, D.B. (2001) “Iterative Automated Record Linkage Using Mixture Models,” *Journal of the American Statistical Association* 79, pp.32–41

Larsen, Rubin

- Larsen, M.D. and Rubin, D.B. (2001) “Iterative Automated Record Linkage Using Mixture Models,” *Journal of the American Statistical Association* 79, pp.32–41
- T is sample of pairs from the clerical review region that have been clerically reviewed

Winkler

- Winkler, W.E. “Automatically Estimating Record Linkage False Match Rates,” (2007)
<http://www.census.gov/srd/www/byname.html>

Winkler

- Winkler, W.E. “Automatically Estimating Record Linkage False Match Rates,” (2007)
<http://www.census.gov/srd/www/byname.html>
- T is sample of “pseudo-truth” data: pairs with sufficiently high or sufficiently low weight

Data Preparation

- Files must have matching fields of fixed length and location

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- Matching fields are compared on a character by character basis

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- Matching fields are compared on a character by character basis
- Unnecessary inconsistencies must be removed before matching is done

Basic Preparation

- Consistently encode categorical variables

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 - Sex, race

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 - Sex, race
 - Date, age

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Basic Preparation

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 - Sex, race
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 - Titles: Dr, Dr., Doctor
 - Nicknames: Bill, William
 - Standard words: Co, Co., Cmpny, Company

Basic Preparation, Cont.

- Identify and parse components

Basic Preparation, Cont.

- Identify and parse components
 - Names: last, first

Basic Preparation, Cont.

- Identify and parse components
 - Names: last, first
 - Addresses: number, street, unit

Address Parsing



16 W Main ST APT 16

RR 2 BX 215

Fuller BLDG SUITE 405

14588 HWY 16 W

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Address Parsing



16 W Main ST APT 16

RR 2 BX 215

Fuller BLDG SUITE 405

14588 HWY 16 W



Pre2	Hsnm	Stnm	RR	Box	Post1	Post2	Unit1	Unit2	Bldg
W	16	Main					16		
			2	215					
								405	Fuller
	14588	HWY 16				W			

Business Lists

- Much harder

Business Lists

- Much harder
- May have fewer comparison fields

Business Lists

- Much harder
- May have fewer comparison fields
 - Name

Business Lists

- Much harder
- May have fewer comparison fields
 - Name
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 - Name
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- These may not be unique

Business Lists

- Much harder
- May have fewer comparison fields
 - Name
 - Address
 - Phone
- These may not be unique
- May be difficult to parse

Example of Business Name Parsing



DR John J Smith MD

Smith DRY FRM

Smith & Son ENTP

Example of Business Name Parsing



DR John J Smith MD

Smith DRY FRM

Smith & Son ENTP



Pre	First	Mid	Last	Post1	Post2	Bus1	Bus2
DR	John	J	Smith	MD			
			Smith			DRY	FRM
			Smith		Son	ENTP	

Two Kinds of Standardizer

- Deterministic

Two Kinds of Standardizer

- Deterministic
 - Rule based

Two Kinds of Standardizer

- Deterministic
 - Rule based
- Probabilistic

Two Kinds of Standardizer

- Deterministic
 - Rule based
- Probabilistic
 - Hidden Markov model

Rule-Based Standardizer

- U.S. Census Bureau software

U S C E N S U S B U R E A U

Rule-Based Standardizer

- U.S. Census Bureau software
- Based on extensive expert experience

U S C E N S U S B U R E A U

Rule-Based Standardizer

- U.S. Census Bureau software
- Based on extensive expert experience
- Created for a specific sample space

U S C E N S U S B U R E A U

Hidden Markov Standardizer

- Adaptable to different sample spaces

Hidden Markov Standardizer

- Adaptable to different sample spaces
- Based on training data

Hidden Markov Standardizer Reference

- P. Christen, T. Churches, J.X. Jhu. (2002) “Probabilistic Name and Address Cleaning and Standardization.” *The Australasian Data Mining Workshop*.
<http://datamining.anu.edu.au/projects/linkage.html>

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- T. Churches, P. Christen, J. Lu, J.X. Zhu. (2002) “Preparation of Name and Address Data for Record Linkage Using Hidden Markov Models.” *BioMed Central Medical Informatics and Decision Making*, 2(9),
<http://www.biomedcentral.com/1472-6947/2/9>.

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- FEBRL Project (Freely Extensible Biomedical Record

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Hidden Markov Model

- Identify a finite number of hidden Markov states

Hidden Markov Model

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 - first, last1, last2, mi, prefix, suffix

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 - Coded rules

Hidden Markov Model, Cont.

- Break object into component observations, assign them initial Markov states

Hidden Markov Model, Cont.

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 - “sir”, “mick”, “jagger”, “mbe”

Hidden Markov Model, Cont.

- Break object into component observations, assign them initial Markov states
 - “sir”, “mick”, “jagger”, “mbe”
- Compute the highest probability sequence of hidden states for the given observations

Viterbi Algorithm

- Not feasible to compute probabilities for all possible paths $O(n^l)$

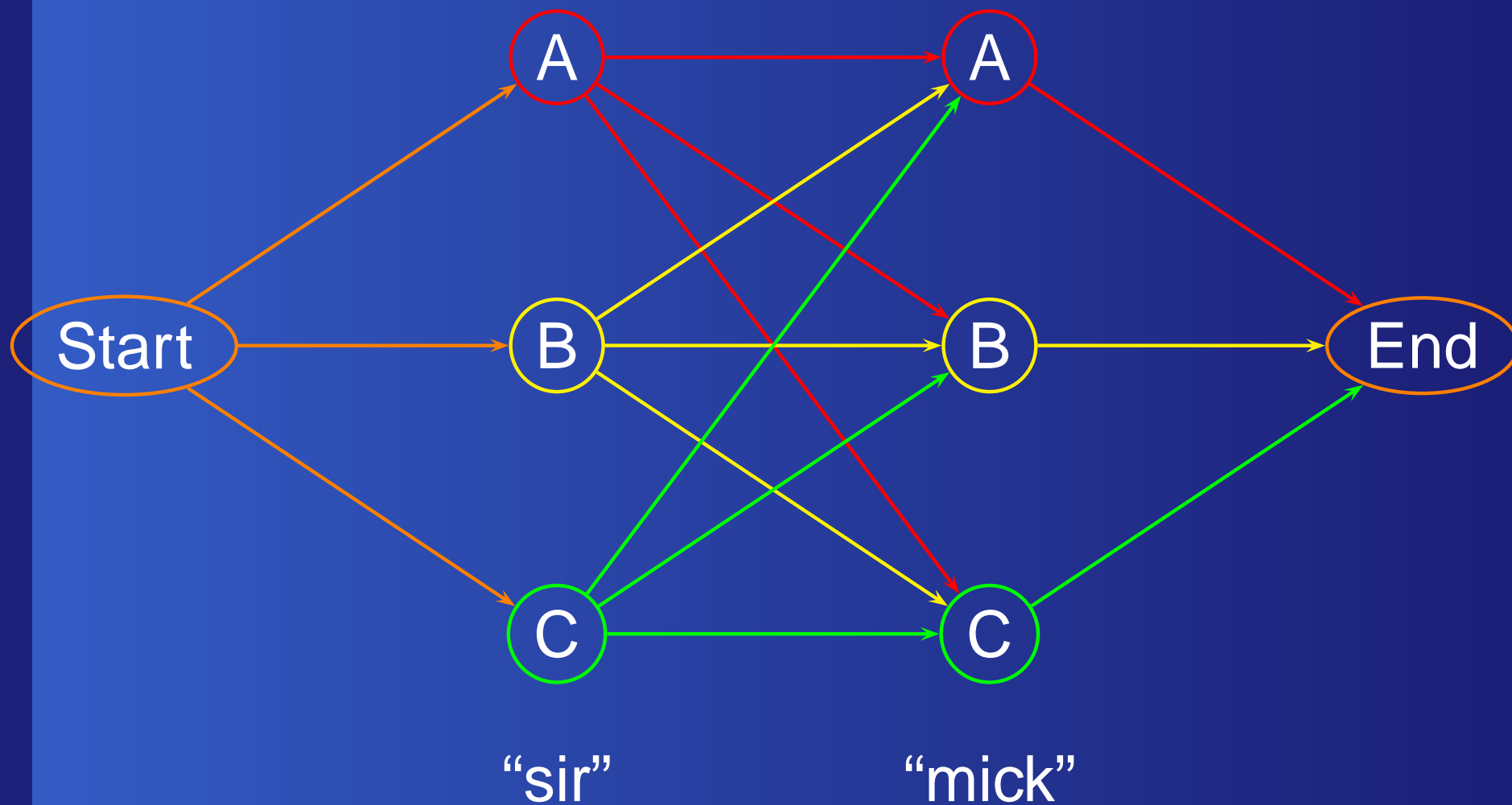
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- Dynamic programming algorithm $O(nl)$

Viterbi Algorithm

- Not feasible to compute probabilities for all possible paths $O(n^l)$
- Dynamic programming algorithm $O(nl)$
- Each state is arrived at by the most probable subpath (Markov property)

HMM Diagram



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Standardization Summary

- Much more time is likely to be spent preparing the data than performing the record linkage

Standardization Summary

- Much more time is likely to be spent preparing the data than performing the record linkage
- Records that fail to be standardized will probably fail to be matched

U.S. Census Bureau Software

- Matching programs

U S C E N S U S B U R E A U

U.S. Census Bureau Software

- Matching programs
 - Matcher

U S C E N S U S B U R E A U

U.S. Census Bureau Software

- Matching programs
 - Matcher
 - Bigmatch

U S C E N S U S B U R E A U

U.S. Census Bureau Software

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- Auxiliary programs

U S C E N S U S B U R E A U

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 - Counter

U S C E N S U S B U R E A U

U.S. Census Bureau Software

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 - EM

U S C E N S U S B U R E A U

U.S. Census Bureau Software

- Matching programs
 - Matcher
 - Bigmatch
- Auxiliary programs
 - Counter
 - EM
 - Standardizer

U S C E N S U S B U R E A U

Matching Programs: Matcher

Matcher

Matching Programs: Matcher

- Matcher
 - One-to-one matching

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 - Files should not have duplicates

Matching Programs: Matcher

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 - Pre-sort files according to blocking scheme

Matching Programs: Matcher

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 - Files should not have duplicates
 - Pre-sort files according to blocking scheme
 - Can re-run program on residual files

Matching Programs: Matcher

■ Matcher

- One-to-one matching
 - Files should not have duplicates
- Pre-sort files according to blocking scheme
- Can re-run program on residual files
 - Resort files according to new blocking scheme

Matching Programs: Bigmatch

■ Bigmatch

Matching Programs: Bigmatch

- Bigmatch
 - No one-to-one matching

Matching Programs: Bigmatch

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 - No one-to-one matching
 - Can be used for deduplicating file

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 - Can match several files to one file

Matching Programs: Bigmatch

- Bigmatch
 - No one-to-one matching
 - Can be used for deduplicating file
 - Do not pre-sort files
 - Can run several blocking schemes
 - Can match several files to one file
 - One file must fit into memory

Auxiliary Programs: Counter

- Counter program

Auxiliary Programs: Counter

- Counter program
 - Simplified matching program

Auxiliary Programs: Counter

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 - Counts number of times each matching pattern occurs

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 - String comparator has (high) cutoff

Auxiliary Programs: Counter

- Counter program
 - Simplified matching program
 - Counts number of times each matching pattern occurs
 - String comparator has (high) cutoff
 - Provides input for EM

Auxiliary Programs: EM

- EM algorithm program

Auxiliary Programs: EM

- EM algorithm program
 - Estimates probability parameters for given file and blocking scheme

Auxiliary Programs: EM

- EM algorithm program
 - Estimates probability parameters for given file and blocking scheme
 - Has 2-class and 3-class versions

Auxiliary Programs, Standardizer

- Standardizer

Auxiliary Programs, Standardizer

- Standardizer
 - Standardizes names and addresses

Auxiliary Programs, Standardizer

- Standardizer
 - Standardizes names and addresses
 - Rule-based parsing