# Record linkage of national laboratory data in South Africa: a novel platform for HIV policy evaluation

### **Jacob Bor**

with William MacLeod, Katia Oleinik, Sue Candy, Mhairi Maskew, Matthew Fox, Cornellius Nattey, Brendan Maughan-Brown, James Potter, Wendy Stevens, Ian Sanne, Sergio Carmona

February 2, 2018 NSF Big Data Hubs "Data Sharing and Cyberinfrastructure Working Group"

Health Economics and Epidemiology Research Office HER<sup>2</sup>RO Wits Health Consortium University of the Witwatersrand



BOSTON

UNIVERSITY

- Large chronic disease epidemics worldwide
- Health systems challenge
- Key role of data to manage care and inform policy



- HIV is a manageable chronic disease
- 37M people with HIV globally; 7M in South Africa
- Lifetime daily antiretroviral therapy (ART)
  - Near-normal life expectancy
  - Treatment-as-prevention
- New and ambitious paradigm: <u>'treat all' to end AIDS</u>
  - South Africa moved to 'treat all' in Sept 2016



# A major challenge



Currently, no dataset provides a system-wide, longitudinal perspective on the HIV care cascade

- National Health Laboratory Service (NHLS) is the sole provider for South Africa's national HIV program
- Longstanding BU-HE<sup>2</sup>RO-NHLS collaboration
- ~40 million CD4, VL results, 2004 May 2015
- >300 million lab tests results in full database
- High quality data; continuously-updated; system-wide
- No unique patient ID...



# Can we build a National HIV Cohort from routine laboratory data?



## **Collaboration between:**

National Health Laboratory Services, South Africa

Health Economics and Epidemiology Research Office, University of Witwatersrand, South Africa

Boston University

- Departments of Global Health and Epidemiology
- Research Computing Services, Shared Computing Cluster
- Hariri Institute for Computing and Computational Science



#### INPUT

· Lab episodes, with identifying information



#### 1. Pre-process data Cleaning Standardization Reduction to exact matches on first/last/DOB/sex/facility 2. Search for edges • Exact match on inversions. multiple names, nicknames Fuzzy matching within blocks to reduce comparisons 3. Score edges Jaro-Winkler string comparisons for names • Fellegi-Sunter similarity

#### 4. Link + resolve entities

- Thresholds for matches
- Transitivity
- Graph-based techniques

#### OUTPUT

- Unique Patient Identifier (BU\_uniq\_ID)
- Cluster characteristics for sensitivity analysis

## 1. Pre-process data

- Cleaning
- Standardization
- Reduction to exact matches on first/last/DOB/sex/facility

#### INPUT

· Lab episodes, with identifying information



#### Cleaning Standardization Reduction to exact matches on first/last/DOB/sex/facility 2. Search for edges Exact match on inversions. multiple names, nicknames Fuzzy matching within blocks to reduce comparisons

#### 3. Score edges

· Jaro-Winkler string comparisons for names • Fellegi-Sunter similarity

scores Optimized weights

#### 4. Link + resolve entities

- Thresholds for matches
- Transitivity
- · Graph-based techniques

#### OUTPUT

- Unique Patient Identifier (BU\_uniq\_ID)
- · Cluster characteristics for sensitivity analysis

## **2. Search for edges**

- •Exact match on inversions, multiple names, nicknames
- •Fuzzy matching within blocks to reduce number of comparisons
- Multiple blocking passes



· Lab episodes, with identifying information



## 3. Score edges

Jaro-Winkler string comparisons

Fellegi-Sunter similarity scores

 $sim_k = log_2(m_k/u_k)$  if match =  $log_2((1-m_k)/(1-u_k))$  if not match

totsim =  $\Sigma w_k^* sim_k$ 

### w<sub>k</sub> optimized using training data

- Unique Patient Identifier (BU\_uniq\_ID)
- Cluster characteristics for sensitivity analysis



- Decision rule for matches
- Transitivity

## **Traditional approach**



- Unique Patient Identifier (BU\_uniq\_ID)
- Cluster characteristics for sensitivity analysis



#### **Graph-based entity resolution**



- Unique Patient Identifier (BU\_uniq\_ID)
- Cluster characteristics for sensitivity analysis



### **Graph-based entity resolution**







- Unique Patient Identifier (BU\_uniq\_ID)
- Cluster characteristics for sensitivity analysis



- Thresholds for matches
- Transitivity
- Graph-based techniques

### **Graph-based entity resolution**

Ongoing: Hariri Research Award to develop new graphbased linkage techniques with George Kollios and Lorenzo Orecchia

#### OUTPUT

Μ

- Unique Patient Identifier (BU\_uniq\_ID)
- Cluster characteristics for sensitivity analysis

# Linkage Results



- 38.5 million lab test results (through 2015q1)
- 18.7 million exact matches on first name, last name, date of birth, gender, and facility
- 9.2 million unique patients identified through probabilistic matching techniques

→ "NHLS National Patient Cohort"



# **Cohort Profile**

- 9.2 million people have ever sought care for HIV. About 40% of these are single CD4 counts. Many who test positive never return to care.
- 3.1 million patients were on ART and virologically monitored during 2013-2014. Compares to 3 million reported to be on ART by NDOH.



# **Can South Africa "treat all"?**

**Preliminary findings** 



# Patients are presenting for HIV care earlier in infection than ever before



## But many still present quite late



## Heterogeneity by gender and district



Median CD4 Counts at Presentation, 2014



## "Treat all" will increase ART uptake among patients with CD4>500



# But many patients do not start ART despite being eligible



# Retention on ART is higher than previously thought



# Can South Africa "treat all"?

Perhaps, but further efforts are needed

- To increase early diagnosis and linkage, particularly among men and in some districts
- To increase ART uptake among those offered therapy



# What's next?



# Building a "digital population health" ecosystem from routine laboratory data



from patient to population

# **Extramural support**

## Awarded

 NIH R01 AI115979-01 (Fox/Maskew) – Analysis of National Lab Database to Evaluate the HIV treatment Rollout in South Africa

## Submitted

- NIH R01 (Bor/Fox) Big Data Methods for Real-Time Evaluation of "Treat All" in the Largest HIV Program in the World
- NIH R01 (Fox/Maskew) Improving the Adolescent Transition to and Retention in Adult HIV Care in South Africa: a National View
- NIH DP2 (Bor) Building a 'Digital Population Health' Ecosystem From Routine Laboratory Data
- NIH R21 (Jenkins) Identifying TB transmission hot-spots from routinely-collected laboratory data



# Thank you

jbor@bu.edu

sites.bu.edu/jbor

