### MATCHING INFECTIOUS DISEASE SURVEILLANCE DATA TO IDENTIFY SYNDEMICS IN NEW YORK CITY, 2000–2013

2015 Northeast Epidemiology Conference (New Brunswick, NJ)

Olivia C. Tran, MPH Senior Research Analyst Division of Disease Control

New York City Department of Health and Mental Hygiene

Co-authors: Jvotsna Ramachandran, Li Chen, MPH, Jennifer Fuld, PhD, MA



#### Outline

- Background
- Match Methodology
- · Preliminary Match Results
- · Conclusions and Next Steps



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## Program Collaboration and Service Integration (PCSI)

- CDC NCHHSTP1 initiative
  - Strategic framework to integrate activities across HIV, tuberculosis (TB), syphilis, gonorrhea (GC), chlamydia (CT), hepatitis B virus (HBV), hepatitis C virus (HCV)
- Integrated data to better understand and address interaction of disease
- Integrated services for people with or at risk for multiple diseases
- <sup>1</sup> National Center for HIV/AIDS, Viral Hepatitis, STD and TB Prevention



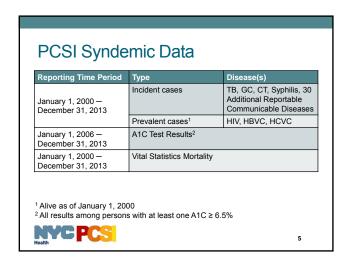
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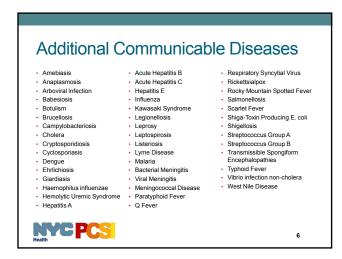
### **PCSI Syndemic Project**

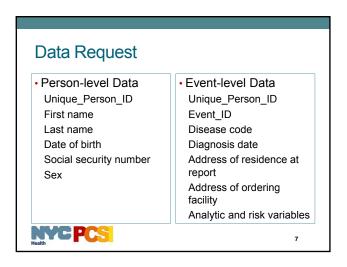
- Retrospective cross match of surveillance data
  - · HIV, TB, syphilis, GC, CT, hepatitis B, hepatitis C
  - 30 additional communicable diseases
  - · NYC vital records mortality data
  - Hemoglobin A1C
- To identify potential disease syndemics in NYC
- Populations at high risk
- Geographic areas with high rates of co-infection

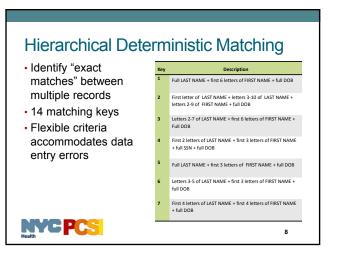


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### Pre-match Data Cleaning

- Ensure variable format consistency (e.g. dates, SSNs)
- Re-purpose 14 match keys to identify potential duplicates within each disease dataset
- Reconcile duplicates in person-level data



### Post-match Data Cleaning and Verification

- De-duplication & Linkage "selection"
  - Two or more individuals could match to the same, single individual in another registry

Disease 1 Unique ID	Disease 2 Link ID	Match Key
X	Z	1
Υ	Z	10



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# Post-match Data Cleaning and Verification (2)

- · De-duplication
  - Two or more individuals could match to the same, single individual in another registry

Disease 1 Unique ID	Disease 2 Link ID	Match Key
Х	Z	1
Υ	Z	10



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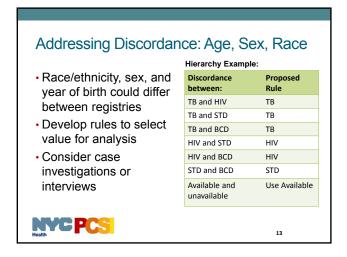
# Post-match Data Cleaning and Verification (3)

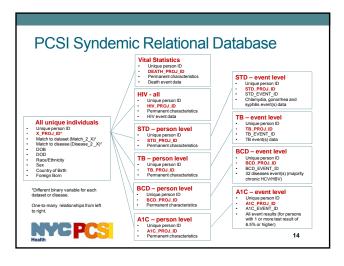
- De-duplication
  - Two or more individuals could match to the same, single individual in another registry

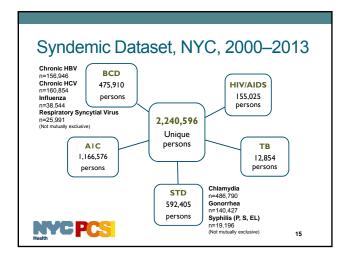
Disease 1 Unique ID	Disease 2 Link ID	Match Key
X	Z	1
V	7	10

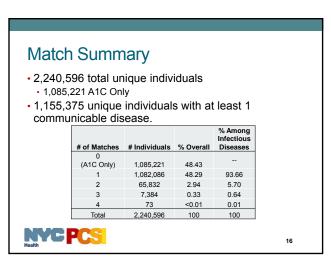


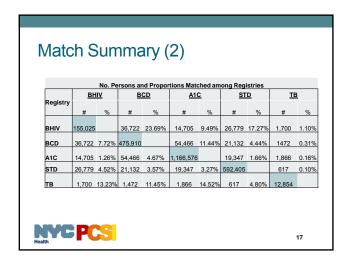
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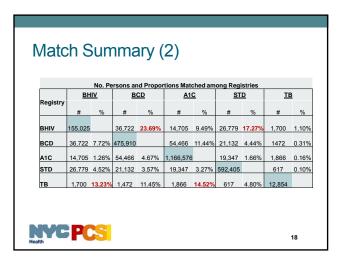


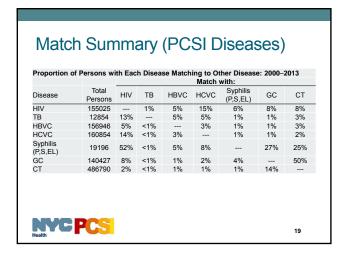


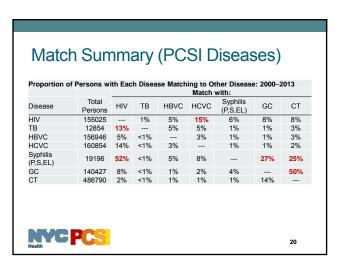












#### **HIV Co-Infection** # persons with # matched to Disease/Infection Tuberculosis HIV 1,700 infected 13.23% Tuberculosis Sexually Transmitted Infection Syphilis (P, S, EL) Gonorrhea Chlamydia Communicable Disease Cryptosporidiosis Hepatitis C (Acute) Strettreesure programming 9 915 1,698 92 12,148 20.65% 19.48% Streptococcus pneumoniae Amebiasis Hepatitis C (Chronic) Hepatitis B (Acute) 6,678 1,218 18.24% 14.98% 14.42% 13.26% 12.64% 11.83% 11.68% 11.49% 160.854 23.227 3,189 14,153 3,426 448 1,877 433 53 6,481 Legionella \* At least one diagnosis of indicated disease

#### Summary

- People living with HIV were most likely to match to other disease registries for sexually transmitted (17.3%) and communicable diseases (23.69%)
- Among people diagnosed with syphilis, more than half (51.65%) are also living with HIV
- HIV is the most common co-infection among people diagnosed with TB (13.23%)
- Diabetes is a co-morbidity among individuals diagnosed with an infectious disease that needs further investigation



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#### **Lessons Learned**

- · Clean data may not be clean
- Event- and person-level data allowed for a more streamlined match while still maintaining data on multiple and/or repeated diagnoses
- De-duplication of data before matching improved results



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### **Next Steps**

- Examine demographic and risk groups most impacted by multiple infections
- Evaluate trends of co-infections over time and by geographic area
- Incorporate additional indicators to understand social determinants of health



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