An Evaluation of Mandatory Communicable Disease Reporting in North Carolina

Emily Elisabeth Vavalle

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Approved by:

David J. Weber, MD, MPH

Jeffrey P. Engel, MD

Pia D.M. MacDonald, PhD

Charles L. Poole, ScD

William A. Rutala, PhD, MPH

Abstract

Emily Elisabeth Vavalle
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(Under the Direction of David J. Weber, MD, MPH)

The current communicable disease surveillance system in the United States largely relies on reporting of communicable diseases and conditions by both physicians and laboratories. Incomplete or inaccurate reporting of these diseases impairs the estimation of incidence rates from surveillance systems as well as hinders the implementation and evaluation of public health control measures. The extent of incomplete reporting has not been quantified for a large geographic area over time or for more than a few diseases. Therefore, the completeness of communicable disease reporting was studied using a retrospective cohort study at 8 large healthcare systems in North Carolina (NC) spanning a ten-year time period. The NC Department of Health and Human Services (NC DHHS) communicable disease surveillance system is based on "mandatory" reporting of more than 60 diseases and conditions and is a passive surveillance system. Diagnostic codes from healthcare system billing records were used to ascertain the eligible cases to be reported to the communicable disease surveillance system, and a unique identifier was used to match these eligible patients to the case-patients who were reported to the NC DHHS surveillance system. In addition, a validation study was also conducted to estimate positive predictive values of the diagnostic codes for communicable disease case ascertainment because these codes are widely used for both public health surveillance and research. Quantification of communicable disease reporting completeness is critical to understanding the impact on two public health surveillance system goals, that is, disease incidence rate estimation and public health initiation of disease transmission control measures. In addition, these analyses may guide the development of local, state and national strategies for improvement of disease reporting and surveillance.

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List of Abbreviations

CDC	Centers for Disease Control and Prevention
CI	Confidence Interval
CSTE	Council of State and Territorial Epidemiologists
DHHS	Department of Health and Human Services
FN	False Negative
FP	False Positive
HIV	Human Immunodeficiency Virus
ICD-9-CM	International Classification of Diseases – 9th Revision, Clinical Modification
NC	North Carolina
NNDSS	National Notifiable Disease Surveillance System
PHE	Public Health Epidemiologist
PPV	Positive Predictive Value
RMSF	Rocky Mountain Spotted Fever
SARS	Severe Acute Respiratory Syndrome
TB	Tuberculosis
TN	True Negative
TP	True Positive
UI	Uncertainty Limits
US	United States

I.   Chapter 1. Background

A. Communicable Disease Surveillance

Surveillance has been defined as the "ongoing systematic collection, analysis and interpretation of outcome-specific data for use in the planning, implementation and evaluation of public health practice" [1, 2]. In the United States, public health surveillance has historically centered on infectious diseases and dates back to 1878 when Congress authorized the Public Health Service to collect morbidity data for cholera, smallpox, plague and yellow fever [3]. Together, the Centers for Disease Control and Prevention (CDC) and The Council of State and Territorial Epidemiologists (CSTE) select the diseases and conditions for mandatory reporting by all states and U.S. territories; currently, there are more than 60 reportable diseases and conditions selected for reporting. However, the exact diseases reported vary somewhat among the states. Communicable disease surveillance data serves a critical role in measurement of endemic incidence of disease in the community, recognition of disease outbreaks, assessment of prevention and control measure effectiveness, allocation of public health resources, and further understanding the epidemiology of new and emerging pathogens [3].

Despite evidence that active surveillance programs such as those that utilize routine telephone and mail contact with physicians have been shown to be 2.6 - 4.8 times more effective than passive disease reporting by physicians [4], most states, including North Carolina, require communicable disease reporting by law [5] but rely solely on passive or voluntary reporting. While passive reporting systems are simple and inexpensive, they have several disadvantages including that the data reported may be highly variable in quality, often incomplete, and not timely [6-47].

Currently in North Carolina, disease reports are initiated on paper communicable disease report forms (Figure 1) and contain demographic, clinical and risk factor data for the case-patient. These reports are required to be submitted to the health department within a specified period of time (i.e., immediately, within 24 hours, or within 7 days) depending on the disease. In all states and U.S. territories, healthcare providers, laboratories or both are assigned responsibility for reporting each case based on standardized case definitions [48]. In a study conducted by CDC and CSTE investigators in 1997, North Carolina had more than 70% concordance with 52 other states and territories for the method of reporting (i.e., physician, laboratory or both) for 34 out of 48 reportable diseases [49]. According to the North Carolina General Statutes [50, 51] communicable disease reporting is required when a physician suspects or confirms that a patient has one of the designated reportable diseases[52]. Other healthcare providers (e.g., nurse practitioners, physician assistants) are not required to report by NC general statutes. The importance of healthcare provider-based reporting is marked by his/her ability to make a diagnosis in the absence of or prior to laboratory confirmation of many diseases and to play a timely role in disease transmission control measures [53]. For many diseases, healthcare providers can serve as an important connection between medicine and public health as they have direct contact with the patient and an ability to provide the health department with detailed information about the patient's illness and risk factors [54].

In addition, in North Carolina since 1998, persons in charge of diagnostic laboratories have also been required to report positive laboratory results for certain diseases [55]. This secondary method of disease reporting was implemented to be a complement but not as a substitute to physician-based communicable disease reporting because many diseases and conditions require clinical correlation in addition to positive laboratory results (e.g., Rocky Mountain Spotted Fever, syphilis). Institution of a dual reporting mechanism (i.e., both physician and laboratory) for many communicable diseases was employed in order to improve completeness, accuracy and timeliness of disease reporting, and duplicate reports are reconciled at the state level. However, the presumed increased effectiveness of a dual reporting mechanism (i.e., laboratories in addition to physicians) has not been comprehensively quantified.

Figure 1. Current Communicable Disease Report Form, Listing of Diseases and Time Within Which Disease Must Be Reported

North Carolina Department of Health and Human Services
Division of Public Health • Epidemiology Section
Communicable Disease Branch • Immunization Branch (WCH Section)

ATTENTION PHYSICIANS/HOSPITALS:
Mail/fax this form to your local health department.

North Carolina
Public Health

Confidential Communicable Disease Report—Part 1

NC DISEASE CODE (see reverse side for code)	DATE OF SYMPTOM ONSET

Patient's First Name | Middle | Last | Suffix | Maiden/Other | Alias

Birthdate (mm/dd/yyyy) | Sex ☐M ☐F ☐Trans. | Parent or Guardian (of minors) | Patient Identifier / SSN

Patient's Street Address | City | State | ZIP | County | Phone (   )   -

Age | Age Type ☐Years ☐Months ☐Weeks ☐Days | Race (check all that apply): ☐White ☐Black/African American ☐American Indian/Alaska Native ☐Native Hawaiian or Pacific Islander ☐Asian ☐Other ☐Unknown | Ethnic Origin ☐Hispanic ☐Non-Hispanic | Initial Source of Report to Public Health: ☐Health Care Provider (specify): ☐Hospital ☐Private clinic/practice ☐Health Department ☐Correctional facility ☐Laboratory ☐Other

Name: ____
Contact Person/Title: ____
Phone: (   )   -   Fax (   )   -
Date Local Health Department Notified: ____

Was patient hospitalized for this disease? (>24 hours) ☐Yes ☐No | Did patient die from this disease? ☐Yes ☐No | Is the patient pregnant? ☐Yes ☐No

Patient is associated with (check all that apply):
☐Child Care (child, household contact, or worker in child care)
☐School (student or worker)
☐College/University (student or worker)
☐Food Service (food worker)
☐Health Care (health care worker)
☐Correctional Facility (inmate or worker)
☐Long Term Care Facility (resident or worker)
☐Military (active military, dependent, or recent retiree)
☐Travel (outside continental United States in last 30 days)

Where was disease/condition most likely acquired?
☐In patient's county of residence
☐Outside county, but within NC - County: ____
☐Out of state - State/Territory: ____
☐Out of USA - Country: ____
☐Unknown

Local Health Department Use Only
Is the patient suspected of being part of a common source outbreak? ☐Yes ☐No
Outbreak setting:
☐Restaurant/Retail (name): ____
☐Household (index case): ____
☐Child Care (name): ____
☐Other (specify): ____
☐Community (index case): ____

Local Health Department Use Only
Communicable Disease Nurse or Designee Reporting to DPH:
Name: ____
Phone: (   )   -
Date sent to DPH: ____
Local Health Director's Signature or Stamp Approving Report

CLINICAL INFORMATION
Specify patient symptoms and treatment:

If a sexually transmitted disease, give specific treatment details:
Date patient treated: (mm/dd/yyyy) ____
Medication ____
Dosage ____
Duration ____

DIAGNOSTIC TESTING
LABORATORY TESTING:

Collection Date	Result Date	Type of Test	Specimen Source	Results (include serogroup/type)	Reference Range	Lab Name—City/State

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Diseases and Conditions Reportable in North Carolina

North Carolina General Statute:
§130A-135. Physicians to report.
A physician licensed to practice medicine who has reason to suspect that a person about whom the physician has been consulted professionally has a communicable disease or communicable condition declared by the Commission to be reported, shall report information required by the Commission to the local health director of the county or district in which the physician is consulted.

North Carolina Administrative Code:
10A NCAC 41A.0101 Reportable Diseases and Conditions
(a) The following named diseases and conditions are declared to be dangerous to the public health and are hereby made reportable within the time period specified after the disease or condition is reasonably suspected to exist.

Diseases in BOLD ITALICS should be reported immediately to local health department.

Reportable to Local Health Department Within 24 Hours

DISEASE/CONDITION	NC DISEASE CODE
A-G	
ANTHRAX	3
BOTULISM, FOODBORNE	10
BOTULISM, INFANT	110
BOTULISM, WOUND	111
Campylobacter infection	50
Chancroid	100
Cholera	6
Cryptosporidiosis	55
Cyclosporiasis	63
Diphtheria	8
E. coli infection, shiga toxin-producing	53
Foodborne disease: Clostridium perfringens	11
Foodborne disease: staphylococcal	12
Foodborne disease: other/unknown	13
Foodborne poisoning: ciguatera	130
Foodborne poisoning: mushroom	131
Foodborne poisoning: scombroid fish	132
Gonorrhea	300
Granuloma inguinale	500
H-N	
Haemophilus influenzae, invasive disease	23
Hemolytic-uremic syndrome (HUS)	59
HEMORRHAGIC FEVER VIRUS INFECTION	68
Hepatitis A	14
Hepatitis B, acute	15
HIV/AIDS HIV	900
AIDS	950
Influenza pediatric death (<18 years)	73
Listeriosis	64
Measles (rubeola)	22
Meningococcal disease, invasive	27
Monkeypox	72
NOVEL INFLUENZA VIRUS INFECTION	75
O-U	
Ophthalmia neonatorum	345
Pertussis (Whooping Cough)	47
PLAGUE	29
Poliomyelitis, paralytic	30
Rabies, human	33
Rubella	36
Salmonellosis	38
S. aureus with reduced susceptibility to vancomycin	74
SARS (coronavirus infection)	71
Shigellosis	39
SMALLPOX	69
Syphilis	
primary	710
secondary	720
early latent	730
latent, unknown duration	740
late latent	745
late with symptoms	750
neurosyphilis	760
congenital	790
Tuberculosis	TB
TULAREMIA	43
Typhoid Fever, acute	44
V-Z	
Vaccinia	70
Vibrio infection, other than cholera & vulnificus	55
Vibrio vulnificus	54

Reportable to Local Health Department Within 7 Days

DISEASE/CONDITION	NC DISEASE CODE
A-G	
Brucellosis	5
Chlamydial infection—laboratory confirmed	200
Creutzfeldt-Jakob Disease	66
Dengue	7
Ehrlichiosis, HGA (human granulocytic anaplasmosis)	571
Ehrlichiosis, HME (human monocytic or e. chaffeensis)	572
Ehrlichiosis, unspecified	573
Encephalitis, arboviral, WNV	98
Encephalitis, arboviral, LAC	96
Encephalitis, arboviral, EEE	97
Encephalitis, arboviral, other	9
H-N	
Hantavirus infection	67
Hepatitis B, carriage	115
Hepatitis B, perinatally acquired	116
Hepatitis C, acute	60
Legionellosis	18
Leprosy (Hansen's Disease)	19
Leptospirosis	20
Lyme disease	51
Lymphogranuloma venereum	500
Malaria	21
Meningitis, pneumococcal	25
Mumps	28
Non-gonococcal urethritis	400
O-Z	
PID (chlamydial/gonococcal)	490
Psittacosis	31
Q fever	32
Rocky Mountain Spotted Fever	35
Rubella, congenital syndrome	37
Streptococcal infection, Group A, invasive	61
Tetanus	40
Toxic shock syndrome, non-streptococcal	41
Toxic shock syndrome, streptococcal	65
Trichinosis	42
Typhoid, carriage (Salmonella typhi)	144
Yellow fever	48

Physicians must report these diseases and conditions to the local health department. For diseases and conditions required to be reported within 24 hours, the initial report shall be made by telephone to the local health department, and the written disease report be made within 7 days. The reporting rules and disease report forms can be accessed at:

http://www.epi.state.nc.us/epi/gcdc.html

If you are unable to contact your local health department, call the 24/7 pager for N.C. Communicable Disease Branch: (919) 733-3419

DHHS 2124 (Revised January 2008) EPIDEMIOLOGY

B. Eligible Case Ascertainment Methods

In order to assess the completeness of a surveillance system, an alternate data source must be chosen to identify cases eligible to be reported to the surveillance system. Previous studies have employed a variety of methods to ascertain these eligible cases including active surveillance as well as using various existing data sources such as medical records, discharge diagnosis codes, Medicaid records, death certificates, and laboratory records [8]. Each of these data sources has advantages and disadvantages for use, and in addition, the positive predictive value and sensitivity of the alternate data sources should be considered.   Unfortunately, the sensitivity and positive predictive value of case ascertainment with these alternate methods has not been well studied and has been found to be low. For example, during a community measles epidemic, when active surveillance was conducted via a household cluster survey that identified eligible cases by direct questioning parents of their children's measles disease history and then verified the children's case eligibility by a medical record review, 23% of those reported to have measles were found to have chickenpox on further questioning [6].

A commonly used method for eligible case ascertainment is the use of standardized International Classification of Diseases Ninth Revision-Clinical Modification codes (ICD-9-CM), which are often used on death certificates, in Medicaid records as well as for hospital and outpatient discharge diagnoses. Large healthcare systems employ trained medical coders who review providers' documentation in order to assign the appropriate ICD-9-CM diagnosis code following the patient's discharge or outpatient visit. The designation of ICD-9-CM codes are standardized across healthcare systems and are designed to capture the patient's clinical diagnosis regardless of laboratory confirmation.

However, ICD-9-CM codes have been found to have variable accuracy for both healthcare billing [56] as well as for disease classification [57] due to both coding and physician errors, and have never been comprehensively validated for their use for surveillance. In an overall assess-

ment of the accuracy of ICD-9-CM codes for Medicare claims data, Fisher and colleagues found that diseases coded as infectious and parasitic diseases had 62.6-65.4% agreement with the abstracted hospital data [57]. In addition, the sensitivity of ICD-9-CM codes for five infectious diseases (shigellosis, salmonellosis, giardiasis, hepatitis A and hepatitis B) was only 53% (10/19) for inpatient cases and 7% (15/213) of outpatient cases [58]. Decreased sensitivity of ICD-9-CM codes in both inpatient and outpatient settings has been attributed to laboratory results not available at the time the patient visit was coded and that more complex clinical diagnoses were given priority over infectious disease clinical diagnosis codes.

In addition to low sensitivity of ICD-9-CM for communicable disease surveillance, these codes may have low positive predictive values for communicable disease surveillance for two main reasons. First, an inpatient may have had suspected disease which warranted the assignment of an ICD-9-CM code, but did not meet the specific communicable disease surveillance case definition. For example, the discordance of ICD-9-CM diagnostic codes and active tuberculosis (TB) cases have been explained by the fact that patient was suspected to have active TB at discharge, but the disease was not yet confirmed, the patient had screening (i.e., tuberculin skin test placed) for evaluation of a latent tuberculosis infection, the patient had a history of treated tuberculosis or that the patient had an infection due to another species of *Mycobacterium* [15, 17]. Second, it is possible that the patient was mistakenly coded as having the disease in the absence of or presence of a similar disease. Thirty-three percent of outpatients and 35% of inpatients were found to be incorrectly coded in small validation studies of ICD-9-CM codes for communicable disease surveillance [27, 59]. Only five completeness studies to date have assessed the positive predictive value of ICD-9-CM codes for eligible case ascertainment [7, 15, 17, 27, 45]. A validation of the eligible case ascertainment method is crucial to any study on reporting completeness because methods with low positive predictive value could lead to underestimates of true reporting completeness and methods with low sensitivity could lead to overestimates of true reporting completeness.

In addition to their use for eligible case ascertainment for assessing disease reporting proportions, ICD-9-CM codes have been proposed to be used as adjuncts to existing public health reporting systems [60] and are key data elements of the National Healthcare Survey, National Ambulatory Medical Care Survey, National Hospital Ambulatory Medical Care Survey, and the National Hospital Discharge Survey which are commonly used for surveillance and research purposes [61]. Therefore, quantifying the positive predictive value and sensitivity of ICD-9-CM codes for disease surveillance has utility beyond the validation of their use as an alternate data source for assessing reporting completeness.

C. Disease Reporting Completeness

Monitoring temporal and geographic disease trends requires consistency of disease reporting but not necessarily completeness. However, complete disease reporting is crucial in order to accurately measure and compare disease incidence rates especially as diseases begin to decrease in incidence (e.g., measles, invasive *H. influenzae* disease), to quantify the risk of rare diseases (e.g., malaria, vaccine-associated paralytic poliomyelitis), and to implement immediate disease control measures and prevent further disease transmission (e.g., meningococcal meningitis, pertussis, bioterrorism agents). Surveys of healthcare providers and laboratory personnel have revealed numerous motives for not reporting diseases to the health department. Reasons cited for not reporting include: confusion or lack of awareness over the reporting process (e.g., where, when and which diseases), concerns over confidentiality and privacy of the patient particularly with sexually transmitted infections, inconvenience of reporting or lack of an established system for reporting, perception of the unimportance of disease reporting, lack of incentives or feedback about reporting, assumption that another entity would report, no definitive diagnosis or laboratory confirmation, and that the patient already received treatment or no treatment or preventive treatment exists for the disease [32, 47, 62, 63].   In addition, rarely, if ever, are penalties enforced for a failure or delay of reporting a communicable disease to the health department.

These barriers to disease reporting contribute to incomplete reporting of diseases of public health concern and thereby threaten the utility of the public health surveillance system. For example, amidst a community-wide outbreak, cluster household surveys showed that for measles, a vaccine preventable disease, reporting was as low as 29% in Los Angeles [6]. Although complete reporting of rare diseases in the United States, like malaria, is critical to ensure that the disease is not becoming endemic in the United States; a recent study has shown only 70% reporting completeness for malaria when comparing laboratory records to surveillance data [10]. Meningococcal disease, a serious disease transmitted from person-to-person through respiratory droplets that requires immediate public health control measures for preventive treatment of close contacts to the source case, has been shown to have a reporting completeness as low as 23% based on laboratory records and death certificates in Wisconsin [29].

Unfortunately, interpretation of previous reporting completeness studies is not straightforward. Disease reporting completeness evaluations in the United States have been conducted for only a limited set of diseases with reporting proportion ranges varying considerably; diseases most commonly evaluated include AIDS (reporting proportions: 31-99%) [12, 36-43], tuberculosis (40-99.5%) [11, 12, 15-18], and other sexually transmitted infections such as chlamydia and gonorrhea (0-96%) [12, 24, 32, 33]. Previous studies examining completeness of disease reporting have differed considerably by size of geographic region (e.g., clinics at a single university to multiple states), ranged in study time period (e.g., several months to several years), evaluated different types of reporting systems (e.g., healthcare provider-based passive reporting versus both healthcare provider and laboratory-based passive reporting), and employed various eligible case ascertainment methods (e.g., laboratory records, billing records, active surveillance, death certificates); the key components of each previous study's design and the reporting completeness proportions are shown in Table 1.

Table 1. Summary of Disease Reporting Completeness Studies

Disease	Location	Time Period	Type of Surveillance	Case ascertainment Method	Results: Percentage (Proportion) and 95% Confidence Interval	Reference
AIDS	New York City	January-June 1983	Healthcare provider based, passive	Lab records, log books, autopsy records compared to health dept case reports	93.6% (235/251)	[39]
AIDS	Washington DC, New York City, Boston, Chicago	July-December 1985	Healthcare provider, medical and laboratory records, active	Death certificate review compared to AIDS registries	89% (487/548) 95% CI: (86-91%)	[40]
AIDS	San Francisco Bay Area	1985-1986	NA	Death certificate/ICD9 codes compared to AIDS registry	92% (1171/1273)	[41]
AIDS	South Carolina	January 1986-June 1987	Healthcare provider based, passive	Uniform billing record (UB-82) review compared to health dept case registry	59.5% (91/153)	[42]
AIDS	Oregon	February 1, 1986 to January 31, 1987	Healthcare provider based, passive	Active surveillance with physicians and infection control practitioners, ICD9 codes, death certificates compared to health dept records	64% (56/85)* 95% CI: (54-74%)	[43]
AIDS/HIV	Outpatient clinics at the University of Arizona	June 1986-June 1988	Healthcare provider based, passive	Diagnosis codes (ICD9) compared to health dept records	80% (92/115)	[12]
AIDS	Alabama, Georgia, Los Angeles, Maryland, New Jersey, Washington State	1988	NA	Medical care databases (hospital discharge records, Medicaid claims) compared to AIDS Reporting System	92% (4157/4500)* 95% CI: (89-96%)	[35]
AIDS	San Mateo County, California	January 1989-December 1990	Healthcare provider-based, passive	Discharge diagnosis (ICD9) codes compared to AIDS registry	76% (72/95)	[36]

Disease	Location	Time Period	Type of Surveillance	Case ascertainment Method	Results: Percentage (Proportion) and 95% Confidence Interval	Reference
AIDS	Philadelphia	Before December 31, 1990	NA	Penn Consortium AIDS database compared to health dept records	90.5% (267/295)	[37]
AIDS	San Mateo County, California	January-March 1991	Healthcare provider based, passive	Active surveillance of AZT administration logs, bronchoscopy logs, respiratory therapy logs, and pathology cancer registry compared to AIDS registry	31% (4/13)	[36]
AIDS	Louisiana Massachusetts San Francisco	1994	Healthcare provider and laboratory based, passive	Medical record review, hospital discharge and Medicaid datasets compared to health dept records	99% (2865/2904)* 95% (1285/1353)* 93% (7834/8463)*	[38]
Amebiasis	Outpatient clinics at the University of Arizona	June 1986-June 1988	Healthcare provider based, passive	Diagnosis codes (ICD9) compared to health dept records	17% (1/6)	[12]
Botulism	Outpatient clinics at the University of Arizona	June 1986-June 1988	Healthcare provider based, passive	Diagnosis codes (ICD9) compared to health dept records	0% (0/1)	[12]
Campylobacteriosis	Pittsburgh, Pennsylvania	January 1 to November 26, 2000	Healthcare provider and laboratory based, passive	Automated, electronic laboratory reporting verified by excluding false positive reports and duplicate reports compared to health dept records	68% (25/37)* 95% CI: (49-85%)	[23]
Chlamydia	Outpatient clinics at the University of Arizona	June 1986-June 1988	Healthcare provider based, passive	Diagnosis codes (ICD9) compared to health dept records	0% (0/4)	[12]
Chlamydia	Rural North Carolina County	March-April, July-December 1993	Healthcare provider based, passive	Hospital laboratory data compared to health dept records	55% (87/158)	[32]
Chlamydia	Rural North Carolina County	May-June 1993	Healthcare provider based, active	Hospital laboratory data compared to health dept records	79% (19/24)	[32]

Disease	Location	Time Period	Type of Surveillance	Case ascertainment Method	Results: Percentage (Proportion) and 95% Confidence Interval	Reference
E .coli O157:H7	Pittsburgh, Pennsylvania	January 1 to November 26, 2000	Healthcare provider and laboratory based, passive	Automated, electronic laboratory reporting verified by excluding false positive reports and duplicate reports compared to health dept records	59% (10/17)* 95% CI: (33-86%)	[23]
Giardiasis	Outpatient clinics at the University of Arizona	June 1986-June 1988	Healthcare provider based, passive	Diagnosis codes (ICD9) compared to health dept records	10% (1/10)	[12]
Giardiasis	Hawaii	July 1 to December 31, 1998	Laboratory based, passive	Automated, electronic laboratory reporting verified by excluding false positive reports and duplicate reports compared to health dept records	33% (26/79)* 95% CI: (30-37%)	[13]
Giardiasis	Pittsburgh, Pennsylvania	January 1 to November 26, 2000	Healthcare provider and laboratory based, passive	Automated, electronic laboratory reporting verified by excluding false positive reports and duplicate reports compared to health dept records	59% (13/22)* 95% CI: (39-77%)	[23]
Gonorrhea	Alaska	May 31, 1973-May 31, 1974	NA	Record review of 8 physicians in 3 communities compared to health dept case reports	42% (76/183)	[34]
Gonorrhea	Vermont	1982-1983	Healthcare provider based, passive	Discharge diagnosis (ICD) codes compared to health dept reports	93% (28/30)	[24]
Gonorrhea	Outpatient clinics at the University of Arizona	June 1986-June 1988	Healthcare provider based, passive	Diagnosis codes (ICD9) compared to health dept records	96% (21/22)	[12]
Gonorrhea	3 Emergency Departments in the District of Columbia	2 months in 1989	Healthcare provider based, passive	Medical record review of culture confirmed cases compared to health dept records	91.5% (204/223)	[33]

Disease	Location	Time Period	Type of Surveillance	Case ascertainment Method	Results: Percentage (Proportion) and 95% Confidence Interval	Reference
Gonorrhea	Rural North Carolina County	March-April, July-December 1993	Healthcare provider based, passive	Hospital laboratory data compared to health dept records	72% (80/111)	[32]
Gonorrhea	Rural North Carolina County	May-June 1993	Healthcare provider based, active	Hospital laboratory data compared to health dept records	88% (21/24)	[32]
H. influenzae meningitis	11 acute care hospitals in Washington DC	January 1-June 31, 1971	Healthcare provider based, passive	Discharge records compared to health dept records	32% (7/22)	[11]
H. influenzae, invasive disease	Tennessee	April 1989-June 1992	Healthcare provider based, passive	Active laboratory-based surveillance system compared to health dept records	49% (94/191)	[9]
H .influenzae	Kentucky	1995	NA	ICD9 codes validated to medical record review compared to health dept records	50% (2/4)	[27]
Viral hepatitis	11 acute care hospitals in Washington DC	January 1-June 31, 1971	Healthcare provider based, passive	Discharge records compared to health dept records	11% (31/282)	[11]
Hepatitis non A, non B	Outpatient clinics at the University of Arizona	June 1986-June 1988	Healthcare provider based, passive	Diagnosis codes (ICD9) compared to health dept records	0% (0/15)	[12]
Hepatitis A	Outpatient clinics at the University of Arizona	June 1986-June 1988	Healthcare provider based, passive	Diagnosis codes (ICD9) compared to health dept records	33% (4/12)	[12]
Perinatal Hepatitis B	New York State (excluding NYC)	1991	Healthcare provider and laboratory-provider based, passive	State health department database from newborn screening program compared to local health dept records	83% (313/378)*	[31]
Acute Hepatitis B	Outpatient clinics at the University of Arizona	June 1986-June 1988	Healthcare provider based, passive	Diagnosis codes (ICD9) compared to health dept records	50% (10/20)	[12]

Disease	Location	Time Period	Type of Surveillance	Case ascertainment Method	Results: Percentage (Proportion) and 95% Confidence Interval	Reference
Acute Hepatitis B	Seattle, Washington	June 1994-May 1998	Healthcare provider and laboratory based, passive	Longitudinal Cohort study data from symptomatic seroconverter intravenous drug users compared to health dept records	14.3% (2/14)	[30]
Acute Hepatitis C	Seattle, Washington	June 1994-May 1998	Healthcare provider and laboratory based, passive	Longitudinal Cohort study data from symptomatic seroconverter intravenous drug users compared to health dept records	0% (0/4)	[30]
Leprosy	Outpatient clinics at the University of Arizona	June 1986-June 1988	Healthcare provider based, passive	Diagnosis codes (ICD9) compared to health dept records	0% (0/1)	[12]
Malaria	Tucson, metropolitan Phoenix, Arizona, San Diego and Imperial Counties, California, Albuquerque, Las Cruces, Sante Fe, and Espanola, New Mexico and Houston/Harris County, Cameron County and El Paso, Texas	January 1 to August 21, 1995	NA	Active laboratory surveys compared to health dept records	70% (43/61) 69% (43/62)*	[10]
Measles	Outpatient clinics at the University of Arizona	June 1986-June 1988	Healthcare provider based, passive	Diagnosis codes (ICD9) compared to health dept records	100% (2/2)	[12]
Measles	Los Angeles	1990-1991	Healthcare provider based, passive	Community wide surveys during an outbreak verified with medical record review compared to health dept records	29% (10/35)	[6]

Disease	Location	Time Period	Type of Surveillance	Case ascertainment Method	Results: Percentage (Proportion) and 95% Confidence Interval	Reference
Measles	New York City	1991	Healthcare provider based, passive	Medical record review compared to health dept records	45% (664/1487)	[46]
Meningococcal meningitis	11 acute care hospitals in Washington DC	January 1-June 31, 1971	Healthcare provider based, passive	Discharge records compared to health dept records	50% (3/6)	[11]
Meningococcal Disease	Wisconsin	January 1980-February 1982	Healthcare provider based, passive	Lab records compared to death certificates and health dept case reports	23% (28/120)	[29]
N. meningitidis, invasive disease	Tennessee	November 1989-June 1992	Healthcare provider based, passive	Active laboratory-based surveillance system compared to health dept records	58% (41/71)	[9]
Meningococcal Disease	New York State (excl NYC)	1991	NA	Statewide hospital discharge records (ICD9) compared to health dept records	93% (100/107)	[7]
N. meningitidis	Pittsburgh, Pennsylvania	January 1 to November 26, 2000	Healthcare provider and laboratory based, passive	Automated, electronic laboratory reporting verified by excluding false positive reports and duplicate reports compared to health dept records	58% (5/9)* 95% CI: (30-88%)	[23]
Meningococcal Disease	Maine	2001-2006	Healthcare provider, healthcare facilities and laboratory based, passive	Statewide hospital discharge records (ICD9) with medical record review validation compared to health dept records	98% (42/43)	[45]
Pertussis	Vermont	1982-1983	Healthcare provider based, passive	Discharge diagnosis (ICD) codes compared to health dept reports	40% (6/15)	[47]

Disease	Location	Time Period	Type of Surveillance	Case ascertainment Method	Results: Percentage (Proportion) and 95% Confidence Interval	Reference
Pertussis (Hospitalizations)	United States	1985-1988	Healthcare provider based, passive	Commission on Professional and Hospital Activities-Professional Activities Survey (ICD9 hospitalization codes) compared to CDC surveillance records	32% (4404/13557)*	[28]
Pertussis (Mortality)	United States	1985-1988	Healthcare provider based, passive	National Center for Health Statistics Vital Statistics System (ICD9 codes on death certificates) compared to CDC surveillance records	33% (32/98)*	[28]
Pertussis	Outpatient clinics at the University of Arizona	June 1986-June 1988	Healthcare provider based, passive	Diagnosis codes (ICD9) compared to health dept records	94% (9/14)	[12]
Pertussis	Kentucky	1995	NA	ICD9 codes validated to medical record review compared to health dept records	100% (2/2)	[27]
Poliomyelitis, paralytic (vaccine-associated)	United States	1980-1991	Healthcare provider based, passive	Data from National Vaccine Injury Compensation Program compared to CDC surveillance records	94% (92/98) 80.7% (92/114)*	[26]
Rubella, congenital	United States	1970-1985	Healthcare provider based, passive	National Congenital Rubella Syndrome Registry and Birth Defects Monitoring Program compared to incidence estimate from capture-recapture technique	28% (337/1186)	[25]
Rubella, congenital	Outpatient clinics at the University of Arizona	June 1986-June 1988	Healthcare provider based, passive	Diagnosis codes (ICD9) compared to health dept records	0% (0/1)	[12]
Salmonellosis	11 acute care hospitals in Washington DC	January 1-June 31, 1971	Healthcare provider based, passive	Discharge records compared to health dept records	42% (11/26)	[11]

Disease	Location	Time Period	Type of Surveillance	Case ascertainment Method	Results: Percentage (Proportion) and 95% Confidence Interval	Reference
Salmonellosis	Vermont	1982-1983	Healthcare provider based, passive	Discharge diagnosis (ICD) codes compared to health dept reports	67% (42/63)	[24]
Salmonellosis	Outpatient clinics at the University of Arizona	June 1986-June 1988	Healthcare provider based, passive	Diagnosis codes (ICD9) compared to health dept records	100% (4/4)	[12]
Salmonellosis	Hawaii	July 1 to December 31, 1998	Laboratory based, passive	Automated, electronic laboratory reporting verified by excluding false positive reports and duplicate reports compared to health dept records	50% (102/205)* 95% CI: (48-51%)	[13]
Salmonellosis	Pittsburgh, Pennsylvania	January 1 to November 26, 2000	Healthcare provider and laboratory based, passive	Automated, electronic laboratory reporting verified by excluding false positive reports and duplicate reports compared to health dept records	91% (32/35)* 95% CI: (83-97%)	[23]
Shigellosis	11 acute care hospitals in Washington DC	January 1-June 31, 1971	Healthcare provider based, passive	Discharge records compared to health dept records	62% (21/34)	[11]
Shigellosis	Wisconsin, Illinois, Pennsylvania, Michigan, New York, Georgia, Connecticut, Iowa, Tennessee, New Jersey	1975	NA	Infected, symptomatic patients that consulted a physician compared to patients reported to local health department	21%	[22]
Shigellosis	Oklahoma	January 1-June 30, 1985	Physician and laboratory-based, passive	Laboratory survey compared to health dept case reports	86% (69/80)	[21]
Shigellosis	District of Columbia	January 1, 1978-July 30, 1978	Healthcare provider and laboratory based, passive	Medical record review compared to health dept records	32% (43/136)	[20]

Disease	Location	Time Period	Type of Surveillance	Case ascertainment Method	Results: Percentage (Proportion) and 95% Confidence Interval	Reference
Shigellosis	Outpatient clinics at the University of Arizona	June 1986-June 1988	Healthcare provider based, passive	Diagnosis codes (ICD9) compared to health dept records	64% (10/15)	[12]
Shigellosis	Hawaii	July 1 to December 31, 1998	Laboratory based, passive	Automated, electronic laboratory reporting verified by excluding false positive reports and duplicate reports compared to health dept records	54% (16/30)* 95% CI: (51-54%)	[13]
S. pneumoniae	Hawaii	July 1 to December 31, 1998	Laboratory based, passive	Automated, electronic laboratory reporting verified by excluding false positive reports and duplicate reports compared to health dept records	9% (5/55)* 95% CI (9-9%)	[13]
Syphilis	Outpatient clinics at the University of Arizona	June 1986-June 1988	Healthcare provider based, passive	Diagnosis codes (ICD9) compared to health dept records	79% (23/29)	[12]
Tetanus Mortality	United States	1979-1984	Healthcare provider based, passive	National Center for Health Statistics Vital Statistics System (ICD9 codes on death certificates) compared to CDC surveillance records	40% (129/326)*	[19]
Tuberculosis	11 acute care hospitals in Washington DC	January 1-June 31, 1971	Healthcare provider based, passive	Discharge records compared to health dept records	63% (127/200)	[11]
Tuberculosis, (positive AFB smears or cultures)	Nassau County, NY	1972	Laboratory based, passive	Laboratory survey compared to health dept records	65% (32/49)	[18]
Tuberculosis	Outpatient clinics at the University of Arizona	June 1986-June 1988	Healthcare provider based, passive	Diagnosis codes (ICD9) compared to health dept records	40% (6/15)	[12]

Disease	Location	Time Period	Type of Surveillance	Case ascertainment Method	Results: Percentage (Proportion) and 95% Confidence Interval	Reference
Tuberculosis	Massachusetts	January 1, 1992-June 30, 1996	Healthcare provider and laboratory based, passive	ICD9 code-medical records and pharmacy record review compared to health dept records	81% (35/43)	[17]
Tuberculosis	Massachusetts, New York (excl. NYC), Utah, Washington, San Diego Co, CA; 3 county areas in Florida and New Jersey	1993-1994	NA	Laboratory records, death certificates, discharge records, Medicaid databases, pharmacy databases compared to health dept records	99.5% (2697/2711)	[16]
Tuberculosis	Wisconsin	1995	Healthcare provider based, passive	ICD9 codes with medical record review to verify compared to TB registry	98% (50/51)	[15]
Tuberculosis	Wisconsin	1995	Healthcare provider based, passive	Laboratory survey with medical record review to verify compared to TB registry	98.9% (87/88)	[15]
Vancomycin-resistant *Enterococci* from a sterile body site	Connecticut	1994-1996	Laboratory based, passive	Laboratory and infection control survey compared to health dept records	59% (158/266)	[14]
Vancomycin-resistant *Enterococci*	Hawaii	July 1 to December 31, 1998	Laboratory based, passive	Automated, electronic laboratory reporting verified by excluding false positive reports and duplicate reports compared to health dept records	22% (7/32)* 95% CI: (19-26%)	[13]

* Estimated by capture-recapture methods [64]

NA: information not available

Only two evaluations, to date, have examined reporting proportions for more than five diseases. In Washington D.C., in 1971, discharge diagnostic codes were used from 11 large hospitals and determined the following reporting completeness proportions (i.e., number of cases reported to the health department/total number of cases that occurred in the hospital): viral hepatitis (31/282) 11%, *H.influenzae* meningitis (7/22) 32%, salmonellosis (11/26) 42%, meningococcal meningitis (3/6) 50%, shigellosis (21/34) 62%, and tuberculosis (127/200) 63% [11]. The largest outpatient based study was conducted from 1986-1988 with diagnostic codes from University in Arizona outpatient clinics; completeness proportions for reportable diseases were found to be: hepatitis B (10/20) 50%, measles (2/2) 100%, pertussis (9/14) (64%), hepatitis A (4/12) 33%, salmonellosis (4/4) 100%, shigellosis (10/15) 64% [12].

Because reporting proportions for communicable diseases have not been comprehensively described for all communicable diseases and vary considerably between studies (e.g, measles 29% [6] vs. 100% [12]; salmonellosis 42% [11] vs. 100% [12], a comprehensive study of multiple reportable diseases using a standard methodology is needed to describe and compare disease reporting completeness proportions.

D. Future of Communicable Disease Surveillance

Communicable disease surveillance in North Carolina has recently been enhanced with the creation of the hospital-based Public Health Epidemiologist (PHE) Network. The PHE Network is funded by the CDC Cooperative Agreement for Public Health Preparedness and Response, Focus Area B, Epidemiology and Surveillance Capacity and began in May 2003. The network includes 11 public health epidemiologists who are healthcare system employees funded by the CDC Cooperative agreement, and 1 Public Health Epidemiologist program director who is a state employee funded by the CDC Cooperative agreement. Healthcare systems or networks were chosen to participate in the PHE network based on geopolitical considerations, region, emergency department volume and bed size, and include teaching and non-teaching and public and private hospitals (Table 3). The PHE Network healthcare systems are located in large cities in

North Carolina (i.e., Greenville, Chapel Hill, Winston-Salem, Wilmington, Greensboro, Charlotte, Durham, Asheville, Raleigh, and Fayetteville) and the locations by county are shown in Figure 3. The mission of the hospital-based public health epidemiologist program is to (1) enhance communication between clinicians, hospitals, and the public health system; (2) assist with development of a surveillance method for monitoring and detecting community-acquired infections as well as detection and response to potential bioterror events, and (3) provide education and heighten awareness for diseases of public health importance.

Table 2. List of Healthcare Systems and Statistics

Healthcare System	Hospital Type	Number of Staffed Inpatient Beds	Inpatient Admissions per Year	Outpatient Visits per Year
Pitt County Memorial Hospitals *Greenville, NC*	Non-government, not for profit	755	34432	271246
UNC Health Care *Chapel Hill, NC*	State	690	31322	1155526
Wake Forest University Baptist Medical Center *Winston-Salem, NC*	Non-government, not for profit	978	34800	202021
New Hanover Health Network *Wilmington, NC*	County	658	32736	118262
Moses Cone Health System *Greensboro, NC*	Non-government, not for profit	1324	46482	572806
Carolinas Medical Center *Charlotte, NC*	Hospital District or Authority	1315	64598	1152935
Duke University Medical Center *Durham, NC*	Non-government, not for profit	761	38185	783154
Mission Hospitals *Asheville, NC*	Non-government, not for profit	721	35299	392600
WakeMed Health and Hospitals *Raleigh, NC*	Non-government, not for profit	752	41670	966534
Cape Fear Valley Health System *Fayetteville, NC*	Non-government, not for profit	581	29097	465713
Durham VA Medical Center *Durham, NC*	Veteran's Affairs	232	Not Available	Not Available
Total		8768	388621	6080797

Reference: [65]

Figure 2. Location of Public Health Epidemiologist Network Hospitals
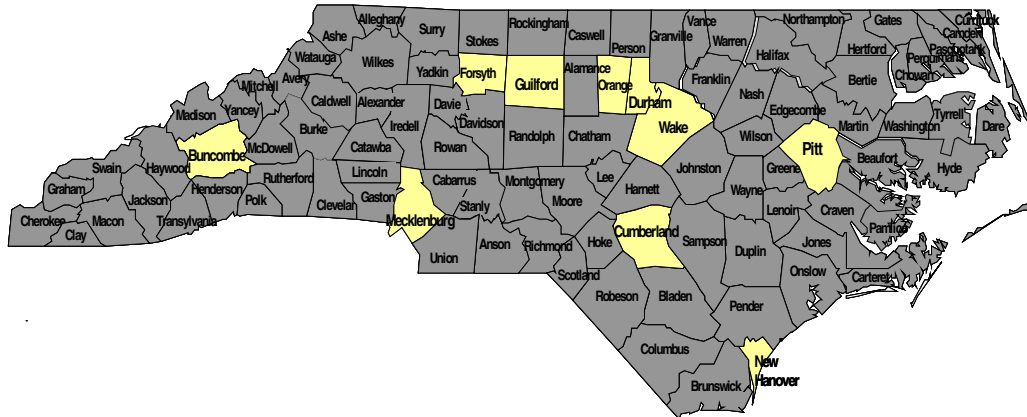
The most recent surveillance innovations are electronic disease reporting and automated disease reporting [66, 67]. Electronic disease reporting and automated disease reporting are terms that are often used interchangeably. Automated disease reporting refers to an active surveillance system that extracts data from medical or laboratory records for reporting and then electronically transmits the data to the health department. Automated reporting does not require physicians' or laboratories' efforts for reporting cases of communicable diseases. In Hawaii, when automated disease reporting was instituted in three statewide private laboratories by extracting data results from the laboratory databases and electronically delivering them to the health department, disease reporting increased 2.3-fold (95% CI 2.0-2.6) and the automated electronic reports were received 3.8 days (95% CI 2.6-5.0) earlier than standard laboratory reporting methods [13]. In Kansas City during a several month long study of automated data reporting from laboratory databases both improved completeness and timeliness of disease reporting were also observed [68].

However, the implementation of these automated reporting systems that employ data extraction methods from laboratory databases for reporting present technical challenges because they rely on standard nomenclature for laboratory results, cannot be easily correlated with clinical diagnoses, and are often difficult to link to databases with patient demographic data needed for public health investigations [69, 70]. In fact, an automated electronic laboratory based reporting

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system in Pittsburgh was found to result in no significant difference in completeness of reporting and a median of only 1 day of improved timeliness compared to the paper-based reporting system; the efficiency of the automated reporting system was reportedly hampered by non-standardized laboratory results (e.g., free text, negation), an inability to retract preliminary reports that were subsequently not confirmed, and low completion rates of patient demographic data fields [23].

Electronic disease reporting is a more general term and without further specification only implies that reporting forms for physicians, laboratories and health departments will be electronic (e.g., web-based) so that communicable disease data forms once completed by a healthcare provider will be transmitted more quickly to the health departments. In 2009, NC began to transition from paper-based to electronic disease reporting. The electronic based disease reporting in NC will occur in several phases--the first phase which was implemented in 2009 involves electronic reporting from the local to the state health department; later phases will incorporate web-based electronic reporting forms for physicians to complete, and only limited automated retrieval of laboratory results is currently planned. The national advent of electronic disease reporting with limited automated reporting is unlikely to drastically improve reporting completeness because even with electronic based reporting mechanisms in place, the communicable disease surveillance system will still remain passive in that reporting will only be accomplished by the medical providers navigating to a secure internet site and entering patient information. Although the ease of reporting is likely to be greatly improved and the transmission time of the data is likely to be reduced with the implementation of electronic reporting technology, the system will continue to rely on medical providers to devote time and effort to complete the reporting.

E.   Conclusion

With the advent of electronic communicable disease reporting underway in NC, it is crucial to describe and understand the impact of communicable disease reporting completeness on this surveillance system.

II.   Chapter 2. Specific Aims

Communicable disease surveillance has been used in the United States since 1878 and is the key method by which states measure endemic incidence of disease in the community, recognize outbreaks of disease, assess the effectiveness of prevention and control measures, allocate public health resources, and further understand the epidemiology of new and/or emerging pathogens. Currently, all states are required to report data on more than 60 notifiable or reportable diseases and conditions to the Centers for Disease Control and Prevention's (CDC) National Notifiable Disease Surveillance System (NNDSS). In North Carolina, communicable disease surveillance is required by law and is based on passive reporting by medical providers and laboratories. Most states, including North Carolina, rely solely on passive reporting for NNDSS. Passive reporting has several disadvantages including that the data reported are highly variable in quality, often incomplete, and not timely. Despite the widespread usage of the NNDSS for public health activities, the completeness of this passive communicable disease reporting system has only been assessed for less than half of the diseases that are reportable by law [6-45], and rarely has a single study included more than 5 diseases [11, 12] or spanned a wide geographic area over time. Further, validation of the case ascertainment method utilized in these studies has rarely been conducted using positive predictive values [7, 15, 17, 27, 45].

Therefore we have:

- Conducted a retrospective cohort study of all inpatients and outpatients who were cared for at the 8 largest healthcare systems in NC during a 10 year time period and who were assigned a diagnostic code corresponding to a reportable communicable disease.

- Reviewed at least 20% of eligible case-patients' medical records from each healthcare system for a one year time period to quantify the positive predictive value of using diagnostic codes for communicable disease case ascertainment.

- Matched eligible patient records from the cohort to the NC DHHS surveillance database of reported communicable disease cases.

- Used semi-Bayesian hierarchical analysis to provide precise estimates of disease reporting completeness and positive predictive values of ICD-9-CM codes for communicable disease surveillance.

Using these methods, we have addressed the following aims:

Aim 1: Determine the positive predictive value (PPV) of diagnostic codes for communicable disease case ascertainment and surveillance. That is, given that a patient is assigned a diagnostic code for a communicable disease, the probability that the patient meets the communicable disease case definition will be determined.

Rationale: Diagnostic codes are commonly used for public health surveillance and research; however the positive predictive value of these codes for communicable disease surveillance has never been well described or quantified. Results from this validation study analysis will improve the interpretation of this study's and other studies' results and may aid in the development of electronic, automated surveillance systems that use diagnostic codes.

Aim 2: Describe the disease-specific completeness of state-required communicable disease reporting, overall state-required communicable disease reporting over a 10 year time period, and overall state-required communicable disease reporting for different healthcare systems.

Rationale: Descriptive epidemiology on the completeness of disease reporting has never been assessed comprehensively for all reportable communicable diseases. Results of these analyses may be used to quantify the completeness of communicable disease case reporting by healthcare providers and to describe the public health impact of incomplete disease reporting.

Aim 3: Utilize hierarchical semi-Bayesian logistic regression analysis techniques to provide more precise estimates of disease-specific reporting completeness and positive predictive values of ICD-9-CM codes.

Rationale: Bayesian analysis has rarely been employed in the field of infectious disease epidemiology. This type of analysis uses hierarchical techniques with variables believed to determine the magnitude of, or explain some variability between, the individual estimates and can be expected to reduce the overall mean squared error when an ensemble of measures are estimated [71].

III.   Chapter 3. Methods

A.   Overall Study Design

A retrospective cohort study was conducted at 8 NC Hospital-Based Public Health Epidemiologist (PHE) network healthcare systems. Both inpatients and outpatients who were assigned discharge diagnostic codes (ICD-9-CM) that correspond with NC reportable communicable diseases during the ten year study time period were included in this retrospective cohort. ICD-9-CM diagnosis codes were chosen as the case ascertainment method for this cohort study based on the standardization of these codes across healthcare systems and for their independence from laboratory confirmation since not all CDC/NC surveillance case definitions require laboratory confirmation of a disease.

The study included two time intervals (Figure 3): 1 January 1995 - 31 December 1997, which represents a time period prior to when laboratories were required by NC law to report positive laboratory results for communicable diseases and when only physicians were required to report by law; 1 January 2000 to 31 December 2006, which represents a time period when both physicians and laboratories were required to report communicable diseases by law, and includes the time periods both before and after the Hospital-based Public Health Epidemiologist (PHE) network was established. The years 1998-1999 are excluded from this study's analysis because the surveillance system in NC was undergoing an important change during this time period as a NC law was passed in August 1998 that required laboratories in addition to physicians to report certain communicable diseases. The PHE network was established in May of 2003, and although the PHEs are not legally required to report communicable diseases, one of their principal roles is to promote communicable disease reporting through education and liaison efforts within the hospitals.

Figure 3. Study Time Intervals
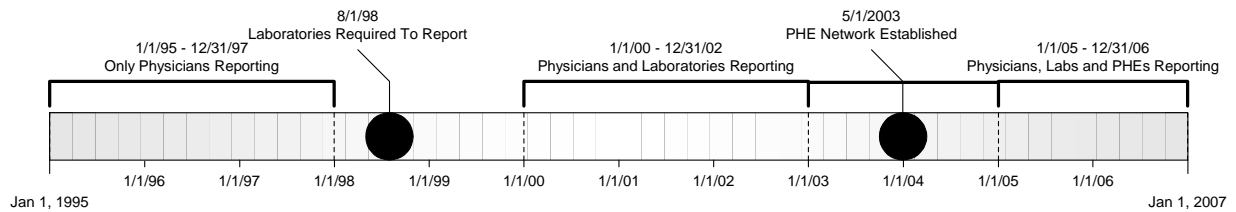
B. Reportable Communicable Diseases

The reportable communicable diseases included in this study are listed in Table 6; these diseases include both nationally reportable diseases and some North Carolina specific diseases (e.g., pneumococcal meningitis). International Classification of Diseases Ninth Revision-Clinical Modification codes (ICD-9-CM) diagnostic codes were selected that are clinically consistent with the CDC communicable disease case definitions [48]. These diagnostic codes were used to query the healthcare system billing records at the 6 participating healthcare systems. Chronic infectious diseases (e.g., HIV, Hepatitis B carrier) were excluded from this study because these diseases were likely to result in a recurring assignment of diagnostic codes when only the initial onset of disease is of interest for incident disease reporting. Diseases for which there is no specific diagnostic code (e.g., monkeypox, viral hemorrhagic fever) were also excluded. In addition, some sexually transmitted infections (e.g., syphilis, chlamydia, gonorrhea) were excluded from the study because NC DHHS did not record patient identifiers for these diseases in their databases during the entire time periods of the study.

Table 3. List of Communicable Diseases Included in Study

Anthrax	Encephalitis, Arboviral (CAL, EEE, WNV, Other)
Botulism	Foodborne Disease: *C. perfringens*
Brucellosis	Foodborne Disease: Staphylococcal
Campylobacter Infection	Hantavirus Infection
Cholera	Hemolytic Uremic Syndrome
Cryptosporidiosis	*Hemophilus influenzae*, Invasive Disease
Cyclosporiasis	Hepatitis A
Dengue	Legionellosis
Diphtheria (Nasopharyngeal only)	Leptospirosis
E.coli, Shiga Toxin-Producing Infection (including *E. coli* O157:H7)	Listeriosis
	Lyme Disease
Ehrlichiosis, Granulocytic	Malaria
Ehrlichiosis, Monocytic (*E. chaffeensis*)	Measles

Meningitis, Pneumococcal
Meningococcal Disease
Monkeypox
Mumps
Plague
Polio, Paralytic
Psittacosis
Q Fever
Rabies, Human
Rocky Mountain Spotted Fever
Rubella
Rubella Congenital Syndrome
Salmonellosis
SARS (Coronavirus infection)
Shigellosis
Smallpox

Streptococcal Infection, Group A, Invasive Disease
Tetanus
Toxic Shock Syndrome
Toxic Shock Syndrome, Streptococcal
Transmissible Spongiform Encephalopathies
(CJD/vCJD)
Trichinoisis
Tuberculosis
Tularemia
Typhoid, Acute
Typhus, Epidemic (louse-borne)
Vaccinia
Vibrio Infection, Other
Vibrio vulnificus
Whooping Cough (Pertussis)
Yellow Fever

C. Healthcare System Databases

The PHE Network hospitals are the 11 largest hospitals or healthcare systems in North Carolina (Table 1). They include 30.6% of all beds in 147 NC hospitals (8,768/28,672 beds), 40.1% inpatient admissions per year at 107 NC hospitals (388,621/968,458 admissions per year), and 32.5% outpatient visits per year at 106 NC hospitals (6,080,797/18,690,065 visits per year) [72]. The benefits of using the healthcare systems in the PHE network are that these healthcare systems are spread geographically throughout the state, account for approximately 30-40% of all inpatient and outpatient visits to healthcare systems in the state, and that the PHE study co-investigators are healthcare system employees who already have access to case-patient records. The use of the PHE network's trained epidemiologists for gathering and reviewing patient records within each healthcare system promotes the internal validity of this cohort study. Eight healthcare systems participated in the overall retrospective cohort study examining the completeness of disease reporting and 6 participated in the chart review validation of ICD-9-CM codes.

Every healthcare system in the PHE network uses electronic records for patient billing. These records include patient demographic data (e.g., name, social security number, address and county of guarantor) and clinical data (e.g., diagnostic codes, procedure codes, admission and discharge dates). Key variables and descriptions are listed in Table 4. In order to query each healthcare sys-

tem patient billing records, a spreadsheet listing of reportable communicable diseases and their corresponding ICD-9-CM codes was prepared and reviewed with each study co-investigator at the participating healthcare systems (Appendix 1). A standardized data request for the medical records department at each healthcare system was prepared by the principal investigator and study co-investigator and contained study inclusion criteria, data elements requested and preferred file formats (Appendix 2).

Table 4. Key Variables in Healthcare System Diagnosis Coding Databases

Variable Name	Description
ADDATE	Admission date or clinic visit date
CO	Patient's county of residence
DCDATE	Discharge date or clinic visit date
DCSTATUS	Patient's discharge status (e.g., Home Routine, Treated Released)
DIAGNOSIS	ICD9-CM code for disease "XXX.XX"
DOB	Patient's date of birth
DXDESC	Text description of ICD9-CM code
DXSEQ	Sequence of diagnostic code
FNAME	Patient's first name
HOSP	Hospital's name
ICU_CARE	Patient with ICU care? Y=Yes N=No
INS	Insurance type (e.g., Medicare, Medicaid, Commercial, etc)
LNAME	Patient's last name
MRN	Patient's medical record number
PTTYPE	Type of patient (i.e., Inpatient, Outpatient, Emergency)
RACE	Patient's race W=White B=Black H=Hispanic O=Other U=Unknown
SEX	Patient's sex M=Male F=Female
SSN	Patient's social security number

Variable Name	Description
SVDATE	Date of clinic visit
YEAR	Year of discharge date for diagnosis

D. NC DHHS Communicable Disease Surveillance Database

During the study time period, NC's communicable disease surveillance data was collected on paper forms that gathered data on demographic, clinical and disease risk factors. Data were re-viewed by the local health department and then mailed to NC DHHS where data were entered into an electronic database. The electronic database contains confirmed, suspect and probable cases ac-cording to standard CDC case definitions [48]. Key variables and their descriptions are listed in Table 5.

NC DHHS study co-investigators provided the health department database of reported commu-nicable diseases required for determining which patients in the study cohort were reported. The da-tabase was queried by year of event (e.g., date of onset) for the designated study time intervals. By querying based on the year of event rather than the year of report, the systematic bias introduced by a right truncation of case-patients diagnosed at the end of the study time period (e.g., a patient diag-nosed on December 31, 2006 and reported on February 15, 2007) were minimized. All available data elements for all included case-patients were transferred from the electronic databases to an electronic file.

Table 5. Key Variables in NC DHHS Surveillance Database

Variable Name	Description
BIRTHDATE	Case's date of birth
CARESITE	Type of Hospital PR=private PU=public

Variable Name	Description
	M=military
CD	Unique numeric code for each communicable disease
COUNTY	Case's county of residence
COUNTDATE	Date entered into state TB database
DIED	Whether case died? 0=No 1=Yes
ETHNIC	Case's Ethnicity H=Hispanic N=Non-Hispanic
EVENTDATE	Date of Communicable Disease (Event type provides further description of this date)
EVENTNAME	Name of Communicable Disease
EVENTTYPE	Type of Communicable Disease Date (in order of preference) 1=Date of Onset 2=Date of Diagnosis 3=Date of Laboratory Diagnosis 4=Date of Report to County 5=Date of Report to State 6=Any Date Associated With Case
FIRST	Case's first name
HOSPITAL	Was case hospitalized? N=No Y=Yes
LASTNAME	Case's last name
MD1STNAME	Reporting physician first name
MDINSTITUT	Reporting physician's institution
MDLASTNAME	Reporting physician last name
RACE	Case's Race B=Black W=White A=Asian O=Other
REPORTDATE (TB cases only)	Date physician or lab reported case or date that the case walked in to local health department
REPORTED	Date case was reported to Local Health Department
REPYEAR	Year of report
SEX	Case's sex M=Male F=Female
SSN	Case's SSN
SUBMITDATE (TB cases only)	Date local health department submitted case to Tuberculosis Consultant
YEAR	Year of report

E. Matching the Healthcare System Database to the Surveillance Database

In order to determine the number of eligible patients that were reported to the NC DHHS's communicable disease surveillance system, persons in the two databases were matched using a unique identifier. Because social security number is the only unique identifier common to the two databases, this variable was used as the primary variable for matching along with a 2-3 digit disease code used administratively by the health department that corresponds to the patient's diagnosis. However, because ~25% of the social security number data was missing in the NC DHHS surveillance database and some healthcare systems did not have social security number data available for this study, a secondary identification variable was created using a combination of the first two letters of the last name, first letter of first name, date of birth and the 2-3 digit administrative communicable disease code. Similar matching algorithms have been utilized in previous studies that required matching two registries. In a study that involved matching TB registries, a matching algorithm that utilized the first two letters of the last name plus the first two letters of the last name plus the month and year of birth and sex, demonstrated a 99% sensitivity and has been shown to be superior to other matching methods including phonetic reduction of names (e.g., Soundex) [73]. Although this created identification variable may not be a truly unique identifier and may be inaccurate if patient's names differ between the two systems, a secondary identification variable was necessary to account for the large number of records with missing social security numbers. Social security number was used first for matching and if social security numbers were not available or no match was achieved with social security number then the created identification variable was used for matching.

The matching process described above matches each healthcare system's records to the NC DHHS surveillance records, so it is possible that a case classified as reported by one facility was actually reported by another facility. The reporting agency name data element (i.e., MDINSTITUT) in the surveillance database is missing in at least ~15% of the case-patient records and is inconsistently

reported with no standardization of the free text entries, so it was not feasible to include this data element as another matching element.

For eligible patients in the hospital database who had more than one visit in a 30-day time period for the same disease, all data elements from the earliest visit were retained and a new variable was created that enumerated the visits for that disease episode. For tuberculosis, this time period was 365 days. For diseases which can only be acquired once – e.g., acute hepatitis A and paralytic polio, only the first instance of the disease was retained. In addition, matching case-patients who had report dates prior to their date of diagnosis at the hospital were excluded as they represented cases already reported to the health department.

Unmatched cases between the two systems should be the result of either (1) the case was not reported, (2) the disease was clinically suspected but did not meet any of the CDC case definitions and therefore the case was not in the state surveillance database or (3) the incorrect assignment of an ICD-9-CM diagnostic code. The possibility of non-matches between the databases due to clinically suspected diseases that did not meet CDC case classification criteria or an incorrect assignment of ICD-9-CM codes were investigated further in the validation study described below.

F. Validation Study Design

Because ICD-9-CM codes were used to query the healthcare system databases to select patients eligible for reporting to the health department, an important source of error is the incorrect assignment of an ICD-9-CM code designated for a communicable disease (i.e., false positives). By assigning ICD-9-CM codes for communicable diseases when the patient has no evidence of a current infection, the actual completeness of reporting will be underestimated. The measurement error associated with these false positive cases, that is the positive predictive value, was quantified by this validation study.

A random sample from a single year (i.e., 2003) of patient records with diagnostic codes for communicable diseases was selected for review at each participating healthcare system. Five patient

records, but at least 20% of case-patient records stratified by disease and by reporting status (i.e., reported case, not reported case) was chosen using random sampling procedures (i.e., PROC SUR-VEYSELECT) within SAS [74]. These patient records were reviewed according the CDC's published surveillance case definitions and determined to be a confirmed case, a suspect case, a probable case or not a case [48]. Those patients who were classified as "not a case" were investigated further to determine the cause for misclassification (e.g., misinterpretation of an abbreviated diagnosis or simi-lar diagnosis, history of disease but not an acute case, clinically compatible case but not consistent with CDC's case definition criteria, no evidence to substantiate diagnostic code) in order to produce a qualitative summarization of these reasons for misclassification.

G. Measurements and Analysis

1. Completeness Study Measurements

The derivation of this cohort study population is shown in Figure 4. The ideal study population for evaluating the completeness of communicable disease reporting in NC is all individuals with re-portable communicable diseases (Population 1); however, only a subset of individuals with reportable communicable diseases are symptomatic (Population 2) and of those, only a subset seek health care for reportable communicable diseases (Population 3). Because it is not feasible to include all North Carolina healthcare facilities in this evaluation, our study population was restricted to those patients who seek healthcare at a PHE network healthcare system (Population 4) and who are then assigned an ICD-9-CM diagnostic code for a reportable communicable disease (Population 5). Population 5 is our study cohort and represents the denominator of the reporting completeness proportions. If all of the patients who are reported to the NC DHHS communicable disease surveillance system are de-fined as Population 6, then the patients who are in the intersection of Populations 5 and 6 represent the reported cases and the numerator of the reporting completeness proportion; which will be desig-nated *a*. Patients who are in Population 5, but not in Population 6 represented the unreported cases, which will be designated *b*. Descriptive analyses of disease-specific, healthcare system specific and overall yearly completeness of communicable disease reporting will be expressed as the proportion of

the diseased patients identified with ICD-9-CM diagnostic codes that were reported to the State

Health Department's communicable disease surveillance system, that is, the completeness proportion

= a / (a+b).

Figure 4. Study Population Derivation
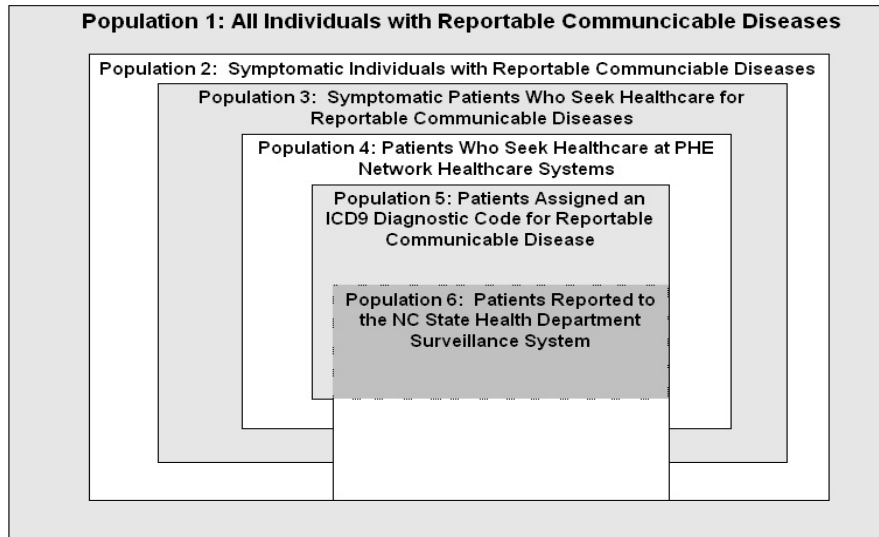
a.   Logit Transformation

Logit transformations (i.e., ln a/b) were used to obtain normally distributed data for the odds of

reporting where *a*= reported cases, *b*=not reported cases.   This transformation yields the following

formulas for reporting completeness proportion, odds, logit and variance of the logit,

reporting completeness proportion = a / (a+b)

reporting completeness odds = a / b

reporting completeness logit = ln (a / b)

variance of reporting completeness logit= (1/a) + (1/b)

After completion of the following analyses, the reporting logit values were converted to reporting pro-

portions using the following calculations:

reporting completeness logit = ln (a / b)

reporting completeness odds = exp (ln (a / b))

reporting completeness proportion = (odds / odds + 1)

    b.   Continuity Corrections

For reporting proportions where *a*, the number of reported cases, is equal to zero, smoothing methods based on those proposed by Sweeting et al were used in order to derive empirical continuity corrections for estimating reporting proportions and uncertainty intervals [75].   The following method was used,

where,

Ω is the pooled logit of all non-zero (a / b) case data weighted by the inverse variance of logit.

$\Omega = \sum \ln (a / b) / [(1 / a)+(1 / b)]$

And,

the continuity corrected reported cases = a + (0.005*Ω)

the continuity corrected unreported cases = b+ [0.005*(1- Ω)]

2.   Hierarchical Semi-Bayesian Regression Methods for Improved Precision

Bayesian methods have been recommended for situations in which multiple comparisons are made [71, 76] and previously have been employed using disease prevalence data (e.g., toxoplasmosis in El Salvador) [71]. Witte proposes using SAS IML code to conduct two stage hierarchical modeling for semi-Bayesian analyses to correct overestimates of observed variance [77].   This procedure serves to shrink unstable estimates towards the mean of the ensemble of estimates. The degree to which estimates are shrunk is proportional to the precision of the estimate (measured in the first-

stage model) and a prespecified variance (tau^2). The resulting group of shrunken estimates should then have a distribution with a variance less than the variance of the distribution of conventional estimates, and this lower variance will outweigh any bias introduced by the shifts [78].

In the first stage of our hierarchical regression model, the continuity corrected logit of disease reporting completeness odds (reported/not reported) is regressed on each specific disease. This first stage model produces the conventional maximum likelihood coefficient and covariance matrix estimates. The second stage model regresses the disease specific maximum likelihood coefficients from the first stage model on a model which contains a matrix of variables believed to determine the magnitude of, or explain some variability between, the individual disease reporting completeness proportions. This matrix is often termed a Z-matrix or an exchangeability matrix. The description of the Z-matrix and the specific values are shown in Tables 6 and 7, respectively. Each exchangeable set of diseases shares information to estimate the final adjusted beta coefficients and standard errors.

Table 6. Description of Exchangeability (Z-matrix) for Disease-Specific Reporting Completeness

Title	Category Description	Hypothesis
Time for Reporting	Is the disease designated to be reported within 24 hours or 7 days?	Diseases required to be reported within 24 hours are more severe, have more public health impact, therefore may be **more likely** to be reported
Reportable by lab	Is the disease required to be reported by the laboratory?	Diseases that are required to be reported by the laboratory in addition to a healthcare provider may be **more likely** to be reported
Serology Lab for Reporting	Does the case definition for the disease require serology lab tests to confirm the disease?	Serology test results usually require multiple tests separated by 2-3 weeks for correct interpretation and these diseases may be **less likely** to be reported
Person-to-Person Transmission	Is the disease transmitted person-to-person?	Healthcare providers' perception of the transmissibility of the disease may make these diseases **more likely** to be reported
Category A Bioterrorism Agent	Is the disease caused by a CDC classified category A bioterrorism agent?	Healthcare providers' perception of the severity of the disease may make these diseases **more likely** to be reported
Arthropod borne	Is the disease arthropod borne?	Healthcare providers' perception of the transmissibility of the disease may make these diseases **less likely** to be reported
Food/ Waterborne	Is the disease transmitted by food/water?	Healthcare providers perception' of the transmissibility of the disease may make these diseases **more likely** to be reported
Aerosol/Droplet Transmission	Is the disease transmitted by aerosol or droplet particles?	Healthcare providers' perception of the transmissibility of the disease may make these diseases **more likely** to be reported

Table 7. Specific Values for the Exchangeability (Z-matrix) for Disease-Specific Reporting Completeness

Disease	Time for Report-ing	Reportable by Lab	Serology Lab for Reporting	Person-to-Person Transmiss-ion	Category A Bioterrorism Agent	Arthropod borne	Food/ Waterborne	Aerosol/droplet Transmission
Anthrax	24 hours	Yes	No	Yes	Yes	No	Yes	Yes
Arboviral Encephali-tis	7 days	Yes	Yes	No	No	Yes	No	No
Botulism	24 hours	Yes	No	No	Yes	No	Yes	No
Brucellosis	7 days	Yes	No	No	No	No	Yes	Yes
Campylobacteriosis	24 hours	Yes	No	Yes	No	No	Yes	No
Cholera	24 hours	Yes	No	Yes	No	No	Yes	No
Creutzfeldt-Jakob Disease	7 days	No	No	Yes	No	No	Yes	No
Cryptosporidiosis	24 hours	Yes	No	Yes	No	No	Yes	No
Cyclosporiasis	24 hours	Yes	No	Yes	No	No	Yes	No
Dengue	7 days	Yes	Yes	No	No	Yes	No	No
Diphtheria	24 hours	Yes	No	Yes	No	No	No	Yes
E.coli O157:H7	24 hours	Yes	No	Yes	No	No	Yes	No
Foodborne Disease, Staphylococcal	24 hours	No	No	No	No	No	Yes	No
Granulocytic Ehr-lichiosis	7 days	Yes	Yes	No	No	Yes	No	No
Hantavirus	7 days	Yes	Yes	No	No	Yes	No	Yes
Hemolytic Uremic Syndrome	24 hours	No	No	No	No	No	No	No
Hemophilus influen-zae, invasive dis-ease	24 hours	Yes	No	Yes	No	No	No	Yes
Hepatitis A, acute	24 hours	Yes	No	Yes	No	No	Yes	No
Legionellosis	7 days	Yes	No	No	No	No	No	Yes
Leptospirosis	7 days	Yes	No	No	No	No	Yes	Yes
Listeriosis	24 hours	Yes	No	Yes	No	No	Yes	No
Lyme Disease	7 days	Yes	No	No	No	Yes	No	No
Malaria	7 days	Yes	No	No	No	Yes	No	No
Measles	24 hours	Yes	Yes	Yes	No	No	No	Yes
Meningococcal men-ingitis	24 hours	Yes	No	Yes	No	No	No	Yes

Disease	Time for Report-ing	Reportable by Lab	Serology Lab for Reporting	Person-to-Person Transmiss-ion	Category A Bioterrorism Agent	Arthropod borne	Food/ Waterborne	Aerosol/droplet Transmission
Monocytic Ehrlicho-sis	7 days	Yes	Yes	No	No	Yes	No	No
Mumps	7 days	Yes	Yes	Yes	No	No	No	Yes
Plague	24 hours	Yes	No	Yes	Yes	No	No	Yes
Pneumococcal men-ingitis	7 days	Yes	No	No	No	No	No	Yes
Poliovirus	24 hours	Yes	No	Yes	No	No	Yes	No
Psittacosis	7 days	Yes	Yes	No	No	No	No	Yes
Q fever	7 days	Yes	Yes	No	No	No	Yes	Yes
Rabies, human	24 hours	Yes	No	No	No	No	No	No
RMSF	7 days	Yes	Yes	No	No	Yes	No	No
Rubella	24 hours	Yes	Yes	Yes	No	No	No	Yes
Rubella Congenital Syndrome	7 days	Yes	Yes	Yes	No	No	No	Yes
Salmonellosis	24 hours	Yes	No	Yes	No	No	Yes	No
SARS	24 hours	No	No	Yes	No	No	No	Yes
Shigellosis	24 hours	Yes	No	Yes	No	No	Yes	No
Smallpox	24 hours	Yes	No	Yes	Yes	No	No	Yes
Streptococcal Infec-tion, group A, inva-sive	7 days	Yes	No	No	No	No	No	No
Tetanus	7 days	No	No	No	No	No	No	No
Toxic Shock Syn-drome	7 days	No	No	No	No	No	No	No
Trichinosis	7 days	Yes	No	No	No	No	Yes	No
Tuberculosis	24 hours	Yes	No	Yes	No	No	No	Yes
Tularemia	24 hours	Yes	No	No	Yes	Yes	Yes	No
Typhoid Fever	24 hours	No	No	Yes	No	No	Yes	No
Typhus, epidemic	7 days	No	No	No	No	Yes	No	No
Vaccinia	24 hours	Yes	No	Yes	No	No	No	Yes
Vibrio vulnificus	24 hours	Yes	No	No	No	No	Yes	No
Vibrio, other	24 hours	Yes	No	No	No	No	Yes	No
Whooping Cough (Pertussis)	24 hours	Yes	Yes	Yes	No	No	No	Yes
Yellow Fever	7 days	Yes	Yes	No	No	Yes	No	No

In addition, a prespecified variance (tau^2) is used in the second stage hierarchical regression. This variance is chosen to incorporate some prior knowledge— maximum likelihood estimates which have previously been the standard in many fields are just a special case of Bayesian analysis where the variance = ∞ and proportion estimates range from 0-100%. However, even by pre-specifying that the likely 95% confidence interval range is from 7-85% rather than 0-100% we are able to obtain more precise estimates. Different values of tau^2 (high tau^2 with 95% CI of 2.2-95%, medium tau^2 with 95% CI of 7-85% low tau^2 with 95% CI of 12.9-75%, zero tau^2 with 95% CI of 35-45%) were tested in the sensitivity analysis. In addition, a sensitivity analysis was conducted on the prior covariates in the Z matrix. Comparisons were made between a model with all prior covariates, no prior covariates and each prior covariate alone. Resultant beta coefficients and standard errors for the odds of reporting were exponentiated and then converted back to proportions using the equation: proportion = odds/(odds+1) to obtain adjusted estimates of proportions and 95% uncertainty limits (UI).

3. **Logistic Regression for Yearly and Healthcare System Specific Disease Reporting Completeness Proportions**

Binomial logistic regression models were utilized to estimate the odds of reporting completeness by year for the three healthcare systems with complete data and by healthcare system for the time period 2000-2006. Resultant beta coefficients and standard errors for the odds of reporting were exponentiated and then converted back to proportions using the equation: proportion = odds/(odds+1) to obtain estimates of proportions and 95% confidence intervals. A generalized linear regression model was used to fit a linear trend line to the graph of reporting proportions by year and these lines were described by their slope and 95% confidence intervals for the slope coefficient. Covariates included for the binomial logistic regression model for healthcare system model included details on how many dedicated staff there are for reporting communicable diseases (i.e., physician, laboratory, infection control and/or PHE). The data on dedicated staff was determined based on a survey completed by all PHE hospitals that consisted of the following four questions. The survey tool is presented below and results of this survey are summarized in Table 8.

1. In your position as the PHE, are you responsible for the actual reporting of new communicable disease cases to the health department? (If yes, go to Q#2) (If no, skip to Q#3)

2. If you are currently responsible for reporting, was someone in your facility's infection control/hospital epidemiology department responsible before the PHE program began? (Go to Q#4)

3. If you are not currently responsible for the reporting, is someone else in your facility's infection control/hospital epidemiology department responsible for the actual reporting of communicable diseases to the health department? (If yes, go to Q#4) (If no, done)

4. If you or infection control/hospital epidemiology do the reporting, are your physicians and laboratories still expected to report too?

Table 8. Healthcare System Dedicated Personnel for Communicable Disease Reporting

Healthcare System	Public Health Epidemiologist	Infection Control	Physician and or Lab
A	Yes	Yes	Yes
B	No	No	Yes
C	Yes	No	Yes
D	Yes	Yes	No
E	No	Yes	Yes
F	No	No	Yes
G	No	No	Yes
H	Yes	No	Yes

4.   Validation Study Measurements

Results of the validation study were summarized as positive predictive value proportions. Disease-specific positive predictive values (PPV) were calculated based on the number of ICD-9-CM disease cases that are determined to be true communicable disease cases based on CDC case definitions, that is the true positives, divided by the total number of reviewed diseased patients identified with ICD-9-CM codes which includes both true positives, TP, and false positives, FP (Table 9).

Table 9. Validation Study Design

		CDC Case Classification	
		Case	Not a Case
ICD-9-CM Code for Communicable Disease	Disease	True Positive (TP)	False Positive (FP)
	No Disease	False Negative (FN)	True Negative (TN)

The estimated positive predictive value for each reporting strata of a disease (i.e., reported, not reported) was combined to obtain an overall disease specific PPV and variance using the sampling weights from each strata using the following formulas. The same procedure was used to combine the disease-specific PPVs across each healthcare system strata.

$$\bar{y}_{strat} = \sum_{k=1}^{K} W_k \ p_k$$

$$var(\bar{y}_{strat}) = \sum_{k=1}^{K} W_k^2 \ S_k^2$$

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where,

K=number of strata

n_k = size of sample from stratum k

N = size of all strata

$W_k = n_k/N$ = the stratum weight

S_k^2 = unbiased estimated variance of proportion= $p_k {}_* q_k / (n_k - 1)$

p_k= estimated positive predictive value

q_k= 1- p_k

Logit transformations and continuity corrections were applied to the positive predictive value of ICD-9-CM codes for communicable disease surveillance as previously described. In addition, hierarchical semi-Bayesian regression methods for improved precision of the disease-specific PPV were utilized as previously described. The description of the Z-matrix for the disease-specific PPVs and the specific values are shown in Tables 10 and 11, respectively.

We chose a tau^2 value of 1.68 that specified a 95% confidence interval range from 10-95% rather than 0-100%. Different values of tau^2 (high tau^2 with 95% CI of 2-99%, low tau^2 with 95% CI of 49-70%, zero tau^2 with 95% CI of 57-63%) were tested. In addition, a sensitivity analysis was conducted on the prior covariates in the Z matrix. Comparisons were made between a model with all prior covariates, no prior covariates and each prior covariate alone. Resultant beta coefficients and standard errors for the odds of reporting were exponentiated and then converted back to proportions using the equation: proportion = odds/(odds+1) to obtain adjusted estimates of proportions and 95% uncertainty limits (UI).

Table 10. Description of Exchangeability (Z-matrix) for Disease-Specific Positive Predictive Values

Title	Category Description	Hypothesis
Reportable by lab	Is the disease required to be reported by the laboratory?	Diseases that have diagnostic laboratory findings may be **more likely** to have an ICD-9-CM code consistent with CDC case definitions.
Serology Lab for Reporting	Does the case definition for the disease require serology lab tests to confirm the disease?	Diseases that have diagnostic laboratory findings may be **more likely** to have an ICD-9-CM code consistent with CDC case definitions.
Rare Disease	Is the disease relatively rare in North Carolina (<10 cases per year)?	Diseases that are relatively common are **more likely** to have an correct assignment of an ICD-9-CM code.

Table 11. Specific Values for the Exchangeability Matrix (Z-matrix) for Disease-Specific Positive Predictive Values

Disease	Reportable by Lab	Serology Lab for Reporting	Rare disease
Arboviral Encephalitis	Yes	Yes	No
Brucellosis	Yes	No	Yes
Campylobacteriosis	Yes	No	No
Cholera	Yes	No	Yes
Creutzfeldt-Jakob Disease	No	No	Yes
Cryptosporidiosis	Yes	No	No
Cyclosporiasis	Yes	No	Yes
Dengue	Yes	Yes	Yes
Diptheria	No	Yes	Yes
E.coli O157:H7	Yes	No	No
Foodborne Disease, Staphylococcal	No	No	No
Granulocytic Ehrlichiosis	Yes	Yes	Yes
Hantavirus	Yes	Yes	Yes
Hemophilus influenzae, invasive disease	Yes	No	No
Hepatitis A, acute	Yes	No	No
Hemolytic Uremic Syndrome	No	No	Yes
Legionellosis	Yes	No	No
Leptospirosis	Yes	No	Yes
Listeriosis	Yes	No	No
Lyme Disease	Yes	No	No
Malaria	Yes	No	No
Measles	Yes	Yes	Yes
Meningococcal meningitis	Yes	No	No

Disease	Reportable by Lab	Serology Lab for Reporting	Rare disease
Monocytic Ehrlichosis	Yes	Yes	No
Mumps	Yes	Yes	Yes
Plague	Yes	No	Yes
Pneumococcal meningitis	Yes	No	No
Poliovirus	Yes	No	Yes
Psittacosis	Yes	Yes	Yes
Q fever	Yes	Yes	Yes
Rabies, human	Yes	No	Yes
RMSF	Yes	Yes	No
Rubella Congenital Syndrome	Yes	Yes	Yes
Rubella	Yes	Yes	Yes
Salmonellosis	Yes	No	No
Shigellosis	Yes	No	No
Smallpox	Yes	No	Yes
Streptococcal Infection, group A, invasive	Yes	No	No
Tetanus	No	No	Yes
Toxic Shock Syndrome	No	No	Yes
Trichinosis	Yes	No	Yes
Tuberculosis	Yes	No	No
Tularemia	Yes	No	Yes
Typhoid, acute	No	No	Yes
Vaccinia	Yes	No	Yes
Vibrio infection, other	Yes	No	Yes
Whooping Cough (Pertussis)	Yes	Yes	No

5.   Limitations of Validation Study

Ideally, the validation study would have provided a measure of both positive predictive value and sensitivity of ICD-9-CM codes for CDC communicable disease case definitions. With both of these of these estimates and using Bayes Theorem, the disease reporting completeness proportions based on ICD-9-CM codes, that is $P(R|I)$, could be adjusted so that they were estimates of the proportion of CDC defined cases who were reported to NC DHHS, that is, $P(R|C)$. The formula for this adjustment is presented below.

Where,

R =Reported to the NC DHHS surveillance system

C =Meets the CDC case definition

I =Assigned an ICD-9-CM code for a communicable disease

$$P(R|C) = \frac{P(C|R)\ P(R)}{P(C)}$$

$$= \frac{P(C|R)\ P(R|I)\ P(I)}{P(C)\quad P(I|R)}$$

$$= \frac{P(C|R)\ P(I|C)\ P(R|I)\ P(I)}{P(C|I)\ P(I)\ \ P(I|R)}$$

$$= \frac{P(C|R)\ P(I|C)\ P(R|I)}{P(I|R)\ P(C|I)}$$

With the following estimates,

P(R|I)=completeness proportions as estimated in this study

P(C|I)= positive predictive values estimated in this study

P(C|R)=1, because all diseases reported are required to meet the CDC case definition

P(I|R)= unknown

P(I|C)= unknown

This study's aims did not include estimates of P(I|R) and P(I|C). These estimates can be further de-

scribed (Figure 5).

Figure 5. 2 x 8 Table of Unmeasured Variables Required for Adjustment

		Reported to NC DHHS	
		Yes	No
ICD-9 Code for Communicable Disease	CDC Disease	A1	B1
	CDC No Disease	C1=0	D1
No ICD-9 Code for Communicable Disease	CDC Disease	A2 (Not Measured)	B2 (Not Measured)
	CDC No Disease	C2=0	D2 (Not Measured)

Where,

P(I|R) = (A1+C1)/(A1+C1+A2+C2) = (A1)/(A1+A2), since C1 and C2=0 because all diseases reported

are required to meet the CDC case definition

and

P(I|C)= (A1+B1)/(A1+B1+A2+B2)

An additional study would need to be designed using an alternate data source such as labora-

tory records or as a true gold standard, complete medical record chart review to obtain estimates of

A2 and B2 for each disease under study. Once these estimates have been obtained, communicable

disease surveillance and study evaluations using ICD-9-CM codes can be adjusted to estimate cases

of communicable diseases as we would like here to appropriately adjust P(R|I) to more accurately

represent P(R|C).

H. Quality Assurance

The major logistical challenge in this study was to obtain 10 years of data from 8 different healthcare systems. Fortunately, the Public Health Epidemiologist (PHE) network facilitated this process as each PHE was committed to participating in this study and are employees of their respective healthcare systems. Each PHE requested data from their healthcare system's medical records department using standardized specifications outlined by the Principal Investigator and PHE Program Director. Ongoing training on these data specifications was provided to the PHEs at training sessions, individual meetings and conference calls. Data from the NC DHHS was requested using written data specifications and obtained from each Branch (i.e., General Communicable Diseases, HIV/STDs, TB) in person by the Principal Investigator. Training on the methods for the chart review involved in validation study was provided to the PHE co-investigators in a written protocol, on conference calls and at training sessions. The standardized data specifications, training sessions for PHE co-investigators and written study protocols helped to assure the quality and consistency of the data collected for analysis.

I. Human Subjects Research

Institutional review board (IRB) approval was obtained at each participating healthcare institution. In addition, a Grant of Public Health Authority has been issued from North Carolina's Department of Public Health to the principal investigator at the sponsoring institution, Emily E. Vavalle of UNC-CH School of Public Health and UNC Health Care System.

This retrospective cohort study included a review of hospital medical records and surveillance records for all eligible patients assigned an ICD-9-CM code for a communicable disease; these patients did not exclude special populations such as pregnant women, children and prisoners. However, patients were not contacted during the course of this study, so no additional precautions were necessary when including these vulnerable populations. Certain protected health information was obtained on each patient in order to conduct this study; these included name, date of birth, and social security numbers. The risks to the study subjects were minimal and the primary concern in this study

was maintaining the confidentiality of the data. Data confidentiality was maintained by restricting access of data to study investigators, storing hard copies of data in locked file cabinets in locked offices, and storing electronic copies of data on password protected, encrypted computers in locked offices. In addition, after completion of matching the hospital and surveillance databases and data analysis, all protected health information will be destroyed. Study subjects will not directly benefit from this research; however, results from this study will be disseminated and used to improve North Carolina's public health surveillance system.

Because thousands of patients were included in this retrospective cohort study using existing medical records and public health surveillance data, informed consent of subjects was impractical due to both the size of the study and the retrospective nature of the data collection. Therefore, we were granted a waiver of the informed consent process and for the Health Insurance Portability and Accountability Act (HIPAA) required documentation for access to healthcare records of the case-patients at each participating healthcare system per each institution's policies.

IV.   Chapter 4: Manuscript "Completeness of Communicable Disease Reporting for 10 Years and For More Than 50 Diseases in Eight North Carolina Healthcare Systems"

A.   Abstract

Context: Communicable disease surveillance is the key method by which states measure endemic disease incidence in the community, recognize disease outbreaks, assess the effectiveness of prevention and control measures, allocate public health resources, and further understand the epidemiology of new and/or emerging pathogens. Despite the widespread usage of surveillance data, the reporting completeness of this system has never been comprehensively assessed. This is the most comprehensive study to date of reporting completeness with an analysis of over 50 diseases and conditions reported by eight healthcare systems across the State of North Carolina during a 10 year time period.

Objective: To describe changes in reporting completeness over time, estimate disease-specific reporting completeness, and examine the variability in reporting between healthcare systems.

Design: A retrospective cohort study was conducted for the years 1995-1997 and 2000-2006.

Setting: Eight acute care healthcare systems in North Carolina which represent 32% of all inpatient visits and 23% of all outpatient visits in NC.

Participants: All inpatients and outpatients who were assigned an ICD-9-CM diagnosis code for a state required reportable communicable disease.

Main Outcome Measure: Semi-Bayesian adjusted disease-specific reporting proportions with 95% uncertainty intervals.

Results: In general reporting completeness improved over time. Disease-specific reporting completeness proportions ranged from 0-82%, but were generally very low. The completeness of reporting varied among the healthcare systems from 2-30%.

Conclusions: Disease reporting completeness based on healthcare facility assigned ICD-9-CM codes was very low even for diseases with great public health importance and opportunity for interventions to prevent person-to-person transmission (e.g., meningococcal meningitis 21.2%). In addition, reporting completeness varied by healthcare system which may be due to healthcare system-specific policies that designate additional person(s) to be responsible for disease reporting, and reporting completeness has increased over time which likely is explained by regulatory and programmatic changes, but it remains very low.

B. Introduction

Surveillance has been the cornerstone of public health since Congress authorized the Public Health Service to collect morbidity data for cholera, smallpox, plague and yellow fever in 1878. Currently, states conduct surveillance of communicable diseases following guidelines from the Centers for Disease Control and Prevention (CDC) and the Council for State and Territorial Epidemiologists (CSTE). The current list of nationally notifiable communicable diseases has expanded to over 60 diseases to include vaccine-preventable diseases (e.g., pertussis, measles), emerging infectious diseases (e.g., SARS, West Nile Virus encephalitis), foodborne diseases (e.g., Shiga toxin-producing *E. coli*, salmonella), sexually transmitted diseases (e.g., syphilis, HIV), as well as aerosol and droplet transmitted diseases (e.g., tuberculosis, meningococcal meningitis). Surveillance on these epidemiologically important diseases provides critical information both to clinicians and public health officials as it is used for the measurement of disease incidence in communities, recognition of disease outbreaks, assessment of prevention and control measure effectiveness, allocation of public health resources, and further understanding the epidemiology of new and emerging pathogens [3].

Like all states, North Carolina (NC) state laws and rules require communicable disease reporting [5, 79, 80] and relies on physicians and laboratories complying with the mandate to report diseases and laboratory results indicative of diseases considered a threat to the public health. During this study's time period, disease reports in NC consisted of paper communicable disease report forms and contained demographic, clinical and risk factor data for the case-patient. These reports are required to be submitted to the health department within a specified period of time (i.e., immediately, within 24 hours, or within 7 days) depending on the disease. An important change to NC Department of Health and Human Service's (NC DHHS) communicable disease surveillance system occurred in September of 1998 when the state administrative code was amended to require that persons in charge of diagnostic laboratories report positive laboratory results for most diseases already reportable by physicians[79]. This dual reporting mechanism was intended to improve completeness, time-

liness and accuracy of surveillance. More recently NC's surveillance efforts have also expanded with the introduction of 7 regional public health teams and 11 hospital-based public health epidemiologists in 2002.

Despite the widespread use of these surveillance data, the systematic collection of these data via mandatory physician and laboratory reporting has never been extensively evaluated. To date, only two evaluations have examined reporting proportions for more than five diseases [11] [12]. Previous studies examining completeness of disease reporting have differed considerably by size of geographic region (e.g., clinics at a single university to multiple states), range of study time period (e.g., several months to several years), heterogeneity of reporting systems (e.g., healthcare provider-based passive reporting versus both healthcare provider- and laboratory-based passive reporting), and various patient ascertainment methods (e.g., laboratory records, billing records, active surveillance, death certificates) rendering the results of these studies difficult to compare or aggregate. Therefore, we have undertaken the most comprehensive study of reporting completeness to date with an analysis of over 50 reportable diseases and conditions in selected healthcare systems across North Carolina during a 10 year time period in order estimate disease-specific reporting proportions, describe changes to reporting over time, and examine the variability of reporting completeness between healthcare facilities.

C. Methods

A retrospective cohort study was conducted at eight large North Carolina (NC) non-federal acute care healthcare systems that make up 32% of all inpatient visits and 23% of all outpatient visits in NC [65]. These healthcare systems ranged from 581 to 1324 site-licensed beds, spanned the Eastern Coastal, Central Piedmont, and Western Mountain regions of the state, and were selected from a network of 11 healthcare systems staffed with hospital-based Public Health Epidemiologists (PHE). The study cohort was defined as all inpatients and outpatients at the eight healthcare systems who were assigned a discharge diagnostic code (ICD-9-CM) that corresponds with a reportable communicable diseases during a ten year study time period (1995-1997, 2000-2006). The years 1998-1999

were excluded from the study because this period marked the transition when the state law changed to include a reporting requirement for laboratories.

Diseases were excluded if they were chronic infectious diseases thus resulting in a recurring assignment of ICD-9-CM code (e.g., HIV, Hepatitis B carrier), if no specific ICD-9-CM code was available (e.g., viral hemorrhagic fever), or if the NC DHHS did not record patient identifiers in their surveillance database during the entire study time period (e.g., syphilis, gonorrhea, chlamydia). Appendix 1 contains a list of diseases and codes used for this study. Approval for the study was granted by the Institutional Review Boards of all healthcare systems as well as the NC Division of Public Health.

The cohort of patients assigned ICD-9-CM diagnostic codes by the healthcare systems for a reportable communicable disease were matched to the NC DHHS reported case-patients using a unique identifier created by either social security number, or a combination of the first two letters of the last name, first letter of the first name, date of birth, and a 2 digit disease code. Repeat patient visits within a 31 day window for the same disease were enumerated and only the first visit was retained with the exception of tuberculosis which had 365 day window. Hepatitis A and paralytic polio were restricted to the first visit since they can only be acquired once in a lifetime. Patients who had dates of reporting to the NC DHHS prior to the date of diagnosis at the healthcare system were excluded as they represented cases which had already been reported.

Unadjusted disease-specific reporting completeness proportions were calculated by dividing the number of case-patients that were reported to NC DHHS by the total number of patients identified in the healthcare systems who were assigned an ICD-9-CM diagnostic code for a reportable disease. In addition, completeness proportions were estimated by year (1995-1997, 2000-2006) for the three healthcare systems that had complete data available for all 10 years and generalized linear regression models were fit to examine the time trends. For the years 2000-2006, reporting completeness proportions and 95% confidence intervals were estimated for each healthcare system using a binomial logistic regression model that included as covariates whether specific healthcare system personnel were designated for disease reporting.

For disease-specific reporting completeness proportions, empirical continuity corrections were used when no patients were reported for a disease [75]. In addition, adjusted completeness proportions and 95% uncertainty intervals were calculated using semi-Bayesian analysis [77] as recommended to reduce the mean squared error when an ensemble of measures are estimated [71]. This semi-Bayesian hierarchical regression analysis utilizes prior covariates that help to explain the mean of the ensemble of estimates as well as a specified prior variance (tau^2) of the distribution. Traditional maximum likelihood estimates (i.e., unadjusted estimates as presented here) can be viewed as a special case of semi-Bayesian analysis in which the prior variance is infinite. By specifying even a moderately informative prior variance such as a tau^2 indicating that 95% of all completeness proportions lie between 7.3% and 85%, an appreciable reduction in the overall mean squared error can be expected with a shift in the point estimate and a narrowing of the 95% uncertainty interval for each completeness proportion, with the relative degree of narrowing being greater for diseases with less information.

A sensitivity analysis was conducted on the specified prior variance (tau^2) using high, medium and low tau^2 values that assumed that 95% of the completeness proportions were within the following ranges: [2.2, 95%], [7.3, 85%], [12.9, 75%]. Sensitivity analyses were also conducted on the inclusion or exclusion of prior covariates which were the time frame for reporting the disease (i.e., 24 hours vs. 7 days), whether or not the disease had a reportable laboratory result, whether or not the disease had reportable serology test results, whether the disease is classified as a CDC category A bioterrorism agent, and the mode of transmission of the disease (person-to-person, arthropod-borne, food/water-borne, droplet/aerosol).

D.   Results

Unadjusted and adjusted disease specific reporting completeness proportions for 2000-2006 with 95% confidence intervals and uncertainty intervals, respectively, are summarized in Table 12. The adjusted disease specific reporting completeness proportions ranged from 0-82.0% and almost all diseases (49/53) had reporting completeness proportions less than 50%. Eleven diseases ac-

counted for 90% of disease reporting: salmonellosis, tuberculosis, meningococcal disease, Rocky Mountain spotted fever, campylobacteriosis, shigellosis, acute hepatitis A, pneumococcal meningitis, legionellosis,malaria and *Hemophilus influenzae*,invasive disease. Some unexpected diseases had patients identified with an ICD-9-CM; for example, anthrax had 14 patients identified, paralytic polio had 32 patients identified, human rabies had 12 patients identified, and smallpox had 9 patients identified. The most dramatic adjustments in the unadjusted to adjusted point estimates were noted for staphylococcal foodborne disease, *Vibrio vulnificus,* and other *Vibrio* infections with ~80% change in point estimate; however, wide uncertainty intervals also reflect the imprecision in these estimates.

Figure 5 displays the overall reporting proportions by year for the two time periods, 1995-1997, when only physicians were required to report most diseases and 2000-2006, when both laboratories and physicians were required to report. Reporting increased significantly in the second time period, but was still very low overall with the linear trend line slope approximately equal to 0 and the intercept equal to 10.2%. Figure 6 displays the reporting proportions by healthcare system for the years 2000-2006. The completeness proportions ranged from 1.8-29.7% with an overall median proportion of 8.0%. The covariates that described whether each healthcare system designated individuals to report had no effect on a healthcare system's reporting proportion.

The sensitivity analysis of the tau^2 values showed that the point estimates and uncertainty intervals (UI) were relatively insensitive to dramatic changes in tau^2; for example, for meningococcal meningitis with a low tau, the reporting proportion and 95% UI was estimated as: 21% (16-28%), with a medium tau, 22% (16-28%); and with a high tau, 22% (16-29%), and the sensitivity analyses examining the use of prior covariates were shown only to have effects on the reporting proportion and 95% UI for diseases with sparse data; for example, cholera with all prior covariates 22% (3-74%), no prior covariates 10% (1-51%), time covariate alone 50% (10-89%).

Table 12. Disease-Specific Reporting Completeness Proportions in NC (2000-2006)

Communicable Disease	Number of Cases Reported to NC DHHS	Number of Patients Identified by ICD-9-CM Code for Reportable Disease	Unadjusted Reporting Completeness Proportion	Lower 95% CI	Upper 95% CI	Semi-Bayesian Adjusted Reporting Completeness Proportion	Lower 95% UI	Upper 95% UI
Anthrax	0	14	0.01%	0.00%	100.00%	0.00%	0.00%	100.00%
Arboviral Encephalitis	0	18	0.00%	0.00%	100.00%	8.67%	0.80%	52.77%
Botulism	0	4	0.02%	0.00%	100.00%	0.08%	0.00%	100.00%
Brucellosis	0	33	0.00%	0.00%	100.00%	23.02%	1.36%	86.62%
Campylobacteriosis	39	97	40.21%	30.94%	50.22%	39.96%	30.82%	49.85%
Cholera	0	6	0.01%	0.00%	100.00%	18.58%	2.24%	69.41%
CJD/vCJD	0	32	0.00%	0.00%	100.00%	0.87%	0.03%	22.97%
Cryptosporidiosis	10	84	11.90%	6.53%	20.73%	12.59%	7.07%	21.42%
Cyclosporiasis	0	3	0.03%	0.00%	100.00%	18.59%	2.25%	69.42%
Dengue	4	25	16.00%	6.14%	35.69%	14.48%	5.92%	31.31%
Diphtheria	0	5	0.02%	0.00%	100.00%	8.28%	0.82%	49.70%
E .coli, Shiga-Toxin Producing	1	3	33.33%	4.34%	84.65%	24.67%	5.82%	63.45%
Foodborne Disease: Staphyloccocal	0	14	0.01%	0.00%	100.00%	74.74%	16.74%	97.76%
Granulocytic Ehrlichiosis	0	67	0.00%	0.00%	100.00%	8.66%	0.80%	52.74%
Hantavirus Infection	0	3	0.03%	0.00%	100.00%	10.10%	0.62%	67.06%
Hemolytic Uremic Syndrome	5	429	1.17%	0.49%	2.77%	2.20%	0.99%	4.84%
Hemophilus Influenzae, Invasive Disease	14	1086	1.29%	0.76%	2.16%	1.45%	0.87%	2.42%
Hepatitis A	27	866	3.12%	2.15%	4.51%	3.34%	2.31%	4.81%
Legionellosis	24	98	24.49%	16.99%	33.95%	24.04%	16.72%	33.27%
Leptospirosis	0	33	0.00%	0.00%	100.00%	23.02%	1.36%	86.62%
Listeriosis	10	64	15.63%	8.62%	26.67%	16.14%	9.12%	26.95%

Communicable Disease	Number of Cases Reported to NC DHHS	Number of Patients Identified by ICD-9-CM Code for Reportable Disease	Unadjusted Reporting Completeness Proportion	Lower 95% CI	Upper 95% CI	Semi-Bayesian Adjusted Reporting Completeness Proportion	Lower 95% UI	Upper 95% UI
Lyme Disease	8	790	1.01%	0.51%	2.01%	1.18%	0.60%	2.30%
Malaria	17	155	10.97%	6.93%	16.94%	10.71%	6.80%	16.47%
Measles	0	14	0.01%	0.00%	100.00%	15.98%	1.41%	71.63%
Meningococcal Disease	38	179	21.23%	15.85%	27.83%	21.19%	15.85%	27.73%
Monocytic Ehrlichiosis	1	4	25.00%	3.35%	76.22%	14.84%	3.12%	48.52%
Mumps	1	96	1.04%	0.15%	7.02%	1.07%	0.20%	5.49%
Plague	0	28	0.00%	0.00%	100.00%	0.00%	0.00%	100.00%
Pneumococcal Meningitis	20	191	10.47%	6.86%	15.67%	10.61%	6.99%	15.80%
Polio, paralytic	0	32	0.00%	0.00%	100.00%	18.56%	2.24%	69.38%
Psittacosis	0	21	0.00%	0.00%	100.00%	17.45%	1.57%	73.69%
Q Fever	3	14	21.43%	7.07%	49.43%	25.68%	9.14%	54.28%
Rabies, Human	0	12	0.01%	0.00%	100.00%	59.69%	8.00%	96.19%
Rocky Mountain Spotted Fever	40	986	4.06%	2.99%	5.48%	4.19%	3.10%	5.66%
Rubella	0	39	0.00%	0.00%	100.00%	15.97%	1.41%	71.61%
Rubella Congenital Syndrome	0	10	0.01%	0.00%	100.00%	1.08%	0.07%	15.32%
Salmonellosis	263	594	44.28%	40.33%	48.30%	44.82%	40.87%	48.83%
SARS (Coronavirus Infection)	0	1	0.08%	0.00%	100.00%	5.71%	0.28%	56.27%
Shigellosis	38	213	17.84%	13.26%	23.57%	18.17%	13.56%	23.93%
Smallpox	0	9	0.01%	0.00%	100.00%	0.00%	0.00%	100.00%
Streptococcal Infection, Group A, Invasive Disease	8	111	7.21%	3.65%	13.75%	7.40%	3.80%	13.92%
Tetanus	1	20	5.00%	0.70%	28.22%	5.25%	1.09%	21.78%
Toxic Shock Syndrome	4	142	2.82%	1.06%	7.26%	3.22%	1.28%	7.83%
Trichinosis	0	23	0.00%	0.00%	100.00%	20.21%	1.82%	77.58%

Communicable Disease	Number of Cases Re-ported to NC DHHS	Number of Patients Identified by ICD-9-CM Code for Reportable Disease	Unadjusted Reporting Completeness Proportion	Lower 95% CI	Upper 95% CI	Semi-Bayesian Adjusted Re-porting Com-pleteness Pro-portion	Lower 95% UI	Upper 95% UI
Tuberculosis	100	1439	6.95%	5.74%	8.38%	7.10%	5.87%	8.55%
Tularemia	0	6	0.01%	0.00%	100.00%	0.04%	0.00%	100.00%
Typhoid, acute	3	12	25.00%	8.28%	55.18%	21.57%	7.49%	48.30%
Typhus, epidemic (louse-borne)	0	2	0.04%	0.00%	100.00%	2.93%	0.12%	42.63%
Vaccinia	0	13	0.01%	0.00%	100.00%	8.27%	0.82%	49.68%
Vibrio Infection, Other	0	1	0.08%	0.00%	100.00%	81.58%	20.46%	98.71%
Vibrio vulnificus	0	2	0.04%	0.00%	100.00%	81.57%	20.45%	98.71%
Whooping Cough (Pertussis)	11	54	20.37%	11.65%	33.16%	20.31%	11.78%	32.72%
Yellow Fever	0	3	0.03%	0.00%	100.00%	8.69%	0.80%	52.81%

Figure 5. Reporting Completeness of Communicable Diseases in NC by Year with 95%
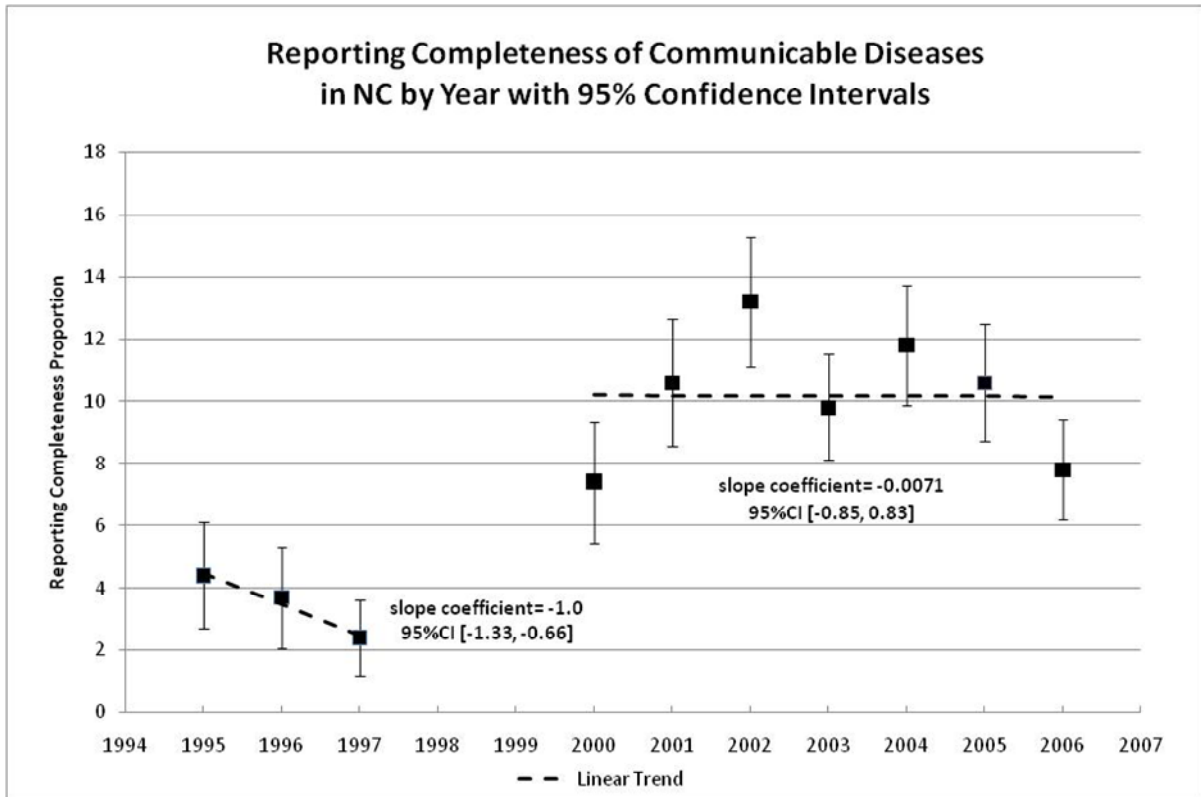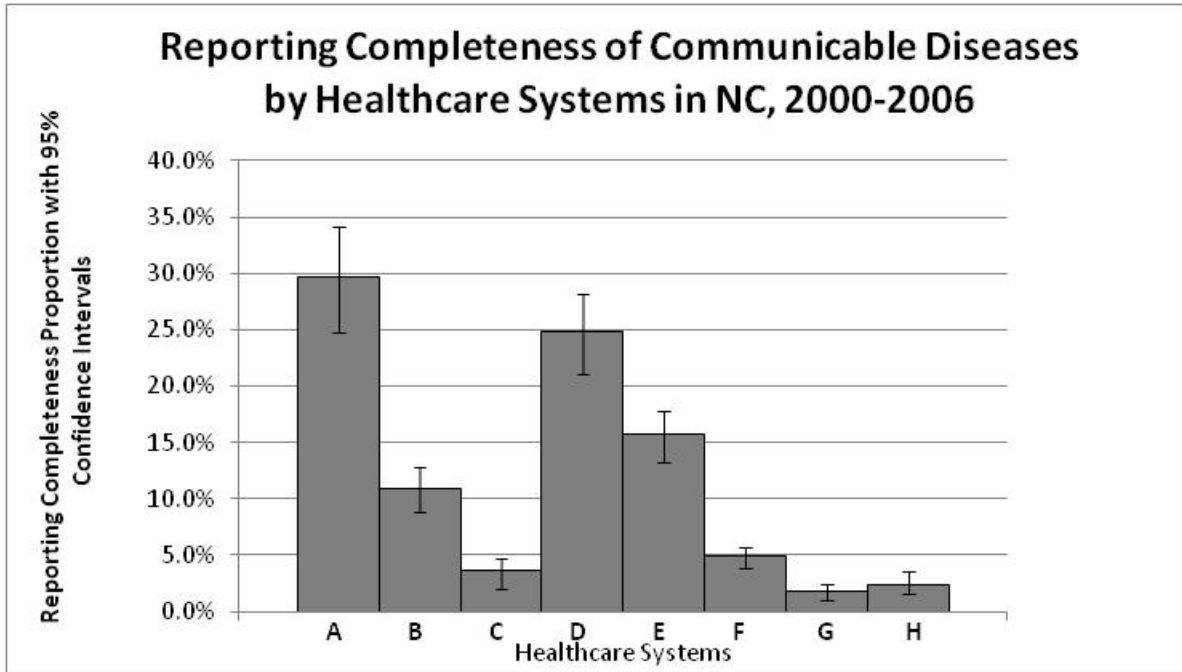
Confidence Intervals

Figure 6. Reporting Completeness of Communicable Diseases in NC Healthcare Systems from

   2000-2006

Reporting Completeness of Communicable Diseases by Healthcare Systems in NC, 2000-2006

E. Comment

The public health surveillance system in North Carolina in this study is similar to surveillance systems utilized nationwide, and although federal funding in addition to state and local budgets support the infrastructure and maintenance of these systems, they are rarely evaluated with respect to the completeness of the communicable disease data reported. North Carolina's population is ranked 11th in the nation based on the 2000 Census, is the seventh largest state east of Mississippi river, and it is diverse enough to experience both exotic communicable diseases (e.g., malaria) as well as routine diseases (e.g., salmonellosis). The size and population diversity allowed for a thorough evaluation of the completeness of many reportable communicable diseases that have rarely been evaluated in previous studies. This study used a trained network of hospital-based Public Health Epidemiologists to gather and review data from existing medical records and existing surveillance databases.

Disease-specific reporting completeness proportions were estimated to be very low and varied greatly based on disease. There are several explanations for variations among disease reporting. First, clinicians may have the perception that some diseases have greater public health threat based on their communicability or morbidity and mortality (e.g., tuberculosis vs. salmonellosis). Secondly, some diseases have relatively straightforward and primarily laboratory-based case definitions (e.g., stool culture positive for *Salmonella* with a clinically compatible illness) whereas others are more complex either requiring multiple laboratory results (e.g., four-fold increase between acute and convalescent serology for Rocky Mountain spotted fever) or a combination of multiple clinical signs and symptoms without any specific laboratory result (e.g. toxic shock syndrome which requires the presence of at least four of the five symptoms: fever, rash, desquamation, hypotension, multisystem involvement). One clear pattern that emerged in our findings was that diseases with fewer clinical criteria and laboratory-based case definitions tended to have higher reporting rates (e.g., salmonellosis 44.8% vs. toxic shock syndrome 3.2%). Laboratory-based case definitions ensure that there is a dual

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reporting system (i.e., both laboratory and physician) and are more straight forward because they require less time reviewing medical records for clinical signs and symptoms. This finding underscores the importance of the simplicity of case definitions, an important attribute in surveillance system development and maintenance.

Notably, we identified some patients by ICD-9-CM diagnostic codes for diseases known to be eliminated in the US (i.e., smallpox and polio). Numerous previous studies which have evaluated reporting completeness have also utilized ICD-9-CM codes [11, 12, 27] as they are standard codes that can be queried relatively easily and should capture clinical cases of disease regardless of laboratory confirmation. The accuracy of the ICD-9-CM codes was a potential limitation in our study. Therefore, we also conducted a validation study of the positive predictive values of ICD-9-CM codes for communicable disease surveillance using as the gold standard complete medical record review. These results showed that for the majority of diseases with higher incidence and relatively straightforward diagnoses, the positive predictive values (PPV) were high (>80%) with the important exception of tuberculosis which had a PPV of 29% (Sickbert-Bennett EE, UNC Gillings School of Global Public Health, unpublished data). For diseases with low PPVs, the estimates we present here are likely to be underestimates of the true reporting completeness. An additional limitation of this study was that we were unable to assess the sensitivity of ICD-9-CM codes for communicable disease reporting. These estimates of sensitivity are required in order to make any adjustments to estimate the true reporting completeness proportion, that is how many cases were reported to NC DHHS divided by the total number of patients with a true reportable disease. Quantification of both the sensitivity and positive predictive values of ICD-9-CM codes for communicable disease surveillance is essential in the interpretation of all ICD-9-CM data as these codes are used frequently for research studies and have been proposed as adjuncts to electronic, automated surveillance systems.

We believe that the semi-Bayesian adjusted estimates offer improved overall accuracy and precision for our ensemble of reporting completeness estimates. Based on our sensitivity analyses, we used a conservative value for our tau^2 with a pre-specified distribution of 7.3%-85% as well as model that included all prior covariates. We did note a dramatic shift in the reporting completeness propor-

tions after semi-Bayesian adjustments for several diseases to include staphylococcal foodborne disease, *Vibrio vulnificus*, and other *Vibrio* infections. This shift reflects both the imprecision in each disease's measured estimates of reporting completeness and the shrinkage of their proportions to others in the same prior covariate group. These three diseases have food/waterborne transmission and therefore their estimates are shrunk towards the mean of the food/waterborne transmission group of diseases which includes many of those with the highest reporting proportion (e.g., campylobacteriosis, salmonellosis). This finding reinforces the importance of careful specification of prior covariates as well as judicious examination and interpretation of unadjusted and semi-Bayesian adjusted estimates along with their precision.

The reporting variation seen in Figure 6 among healthcare systems may be explained in part by healthcare systems' internal policies which assign the responsibility for communicable disease reporting to the infection prevention department. For example, the healthcare system with the highest reporting proportion (Healthcare System A) has hospital-based PHE and/or infection preventionists responsible for disease reporting while the healthcare system with the lowest reporting proportion (Healthcare System G) does not place any responsibility for reporting on the infection preventionists or hospital-based PHE. However, adjusting for these healthcare system policies was not found to modify the healthcare system reporting completeness proportions. Currently, the NC General Statute states that medical facilities *may* report [81] as opposed to physicians and persons in charge of laboratories who *shall* report [51, 82]. Infection prevention departments typically receive laboratory data daily and routinely review medical records. Because infection preventionists are well-trained on the application of case definitions and share disease prevention and control goals with the local health department, they can serve as partners to the local health department in assuring that diseases are reported and investigated appropriately. However, with the existing requirements that physicians and laboratories report these diseases, consideration needs to be given to avoid redundancy in reporting into the surveillance system, which could cause reporting fatigue and the often mistaken assumption that someone else has reported the case-patient [47, 54].

The general trend of the yearly reporting completeness proportions suggests that disease report-ing has improved over time yet remains very low. Several notable changes have occurred in this time period to North Carolina's surveillance system. First, in 1998, the inclusion of laboratory mandated reporting served as a secondary reporting mechanism in addition to the already mandated physician based reporting. Regional public health teams were established in 2002 in order to assist local health departments with outbreak investigations. In 2003, a network of trained hospital-based Public Health Epidemiologists was initiated with their primary role as facilitators of disease reporting and/or investi-gation of cases; also in 2003, a statewide syndromic surveillance system was created to assist in early case identification in the hospitals' emergency departments. Despite the positive effect these regulatory and programmatic changes likely has had on disease reporting, disease reporting remains low as is consistent with other passive reporting surveillance systems.

More recently, automated alerting and data collection for case-patients with reportable diseases (e.g., a positive blood culture result with Gram-negative diplococci triggers an alert with case-patient contact information to infection preventionist and/or local health department staff) has been shown to increase reporting rates when applied to traditional passive surveillance systems [68] [13]. Although North Carolina, like many states, is in the process of developing an electronic disease surveillance system, the reporting of communicable diseases surveillance by physicians will still remain largely passive in that reporting will be accomplished by accessing a secure internet site and entering patient information.

When health information exchange becomes a reality, public health surveillance can benefit sig-nificantly by automating processes that currently rely on manual data entry. Automated disease re-porting could be achieved by standardized queries directly from the electronic health records for key laboratory results (e.g., positive acid-fast bacillus sputum smear) and for simplified or proxy clinical case definitions using ICD-9-CM diagnosis codes or free-text admission diagnoses. Upon recognition of these potential case-patients, automating surveillance data collection directly from electronic health records to populate data fields for basic patient demographics and laboratory results could also sig-nificantly reduce administrative time for physicians and health department officials and expedite dis-ease investigations. This type of automated technology for electronic health records is consistent

with The American Recovery and Reinvestment Act of 2009 which authorizes the Centers for Medicare & Medicaid Services (CMS) to provide reimbursement incentives for healthcare entities who are "meaningful users" of certified electronic health record technology. In fact, the recent draft recommendations for defining "meaningful use" from the Health IT Policy Council to the National Coordinator recommend that hospitals be capable of providing electronic submission of reportable lab results to public health agencies by 2011 [83]. Such an undertaking will require implementation of national laboratory reporting standards for hospitals and could only be accomplished with resource allocation and partnerships between health departments and health care systems. The "meaningful use" of the electronic health record for automated case-finding and data collection will transition our current public health surveillance system from passive to active and thereby overcome the major barriers to complete, accurate and timely communicable disease reporting and surveillance.

V.   Chapter 5: Manuscript "Utility of ICD-9-CM Codes for Infectious Disease Surveillance"

A.   Abstract

International Classification of Diseases Ninth Revision-Clinical Modification (ICD-9-CM) codes have been proposed as a method of public health surveillance and are widely used in public health and clinical research. However, ICD-9-CM codes have been found to have variable accuracy for both healthcare billing as well as for disease classification, and they have never been comprehensively validated for their use for surveillance. Therefore, we undertook the most comprehensive analysis to date of the positive predictive values of ICD-9-CM codes for communicable diseases in 6 healthcare systems in North Carolina. Stratified random samples of patient charts with ICD-9-CM diagnoses for communicable diseases were reviewed and evaluated for their concordance with the Centers for Disease Control and Prevention (CDC) surveillance case definitions. Semi-Bayesian hierarchical regression techniques were employed on our ensemble of disease-specific positive predictive values in order to reduce the overall mean squared error. We found that for the majority for diseases with higher incidence and relatively straightforward laboratory-based diagnoses, the positive predictive values were high (>80%) with the important exception of tuberculosis which had a PPV of 23.6% (95% CI: 15.6, 46.5%).

B. Introduction

International Classification of Diseases Ninth Revision-Clinical Modification codes (ICD-9-CM) codes, used on death certificates, in Medicaid records as well as for hospital and outpatient discharge diagnoses, have been proposed to be used as adjuncts to existing public health reporting systems [60]. In addition, ICD-9-CM codes are key data elements of the National Healthcare Survey, National Ambulatory Medical Care Survey, National Hospital Ambulatory Medical Care Survey, and the National Hospital Discharge Survey which are commonly used for surveillance and research purposes [61]. The benefit of utilizing ICD-9-CM codes for surveillance and research are that they are standardized across healthcare systems, applied in both outpatient and inpatient settings, can be easily queried electronically, and are designed to represent a patient's overall clinical diagnosis as the physician takes into account numerous clinical data (e.g., physical exam findings, laboratory findings, radiological findings).

However, ICD-9-CM codes have been found to have variable accuracy for both healthcare billing [56] as well as for disease classification [57] due to both coding and physician errors. In an overall assessment of the accuracy of ICD-9-CM codes for Medicare claims data, Fisher and colleagues found that diseases coded as infectious and parasitic diseases had 62.6-65.4% agreement with the abstracted hospital data [57]. In addition, the sensitivity of ICD-9-CM codes for five infectious diseases (shigellosis, salmonellosis, giardiasis, hepatitis A and hepatitis B) studied at one medical center was estimated to be only 53% (10/19) for inpatient cases and 7% (15/213) of outpatient cases [58]. Decreased sensitivity of ICD-9-CM codes in both inpatient and outpatient settings has been attributed to laboratory results not available at the time the patient visit was coded and more complex clinical diagnoses were given priority over infectious disease clinical diagnosis codes.

In addition to potentially low sensitivity of ICD-9-CM codes for communicable disease surveillance, some disease codes may also have low positive predictive values. One small validation study of ICD-9-CM codes for communicable disease surveillance found that 33% of outpatients and 35% of inpatients were incorrectly coded [27, 59]. An examination of the discordance between ICD-9-CM

diagnostic codes and active tuberculosis (TB) cases found several explanations for incorrect assign-ment of codes – the patient was suspected to have active TB at discharge, but the disease was not yet confirmed; the patient had screening (i.e., tuberculin skin test placed) for evaluation of a latent tuberculosis infection; the patient had a history of treated tuberculosis; or the patient had an infection due to another species of *Mycobacterium* that was not included in the *M.tuberculosis* complex [15, 17].

Despite these recognized concerns over low sensitivity and low positive predictive value of ICD-9-CM codes for communicable diseases, these codes have never been comprehensively validated for their use for surveillance though they continue to be utilized in both surveillance programs and re-search studies. Therefore, we have undertaken the most comprehensive validation study to date of the positive predictive values for ICD-9-CM codes for communicable disease surveillance.

C.   Materials and Methods

A retrospective cohort study was conducted at 8 large North Carolina (NC) non-federal acute care healthcare systems that make up 32% of all inpatient visits and 23% of all outpatient visits in NC [65] and included both inpatients and outpatients who were assigned discharge diagnostic codes (ICD-9-CM) that correspond to communicable diseases that are reportable in NC (Appendix 1) during a ten-year study time period (1995-1997, 2000-2006). Diseases were excluded if they were chronic infectious diseases thus resulting in a recurring assignment of ICD-9-CM code (e.g., HIV), if no spe-cific ICD-9-CM code was available (e.g., viral hemorrhagic fever), or if the NC Department of Health and Human Services (NC DHHS) did not record patient identifiers in their surveillance database dur-ing the entire study time period (e.g., gonorrhea). Approval for the study was granted by the Institu-tional Review Boards of all healthcare systems as well that of NC DHHS.

Cases were matched from the healthcare system ICD-9-CM records to the NC DHHS surveil-lance database using a unique identifier created by either social security number, or a combination of the first two letters of the last name, first letter of the first name, date of birth, and a 2 digit disease code. Six of the healthcare systems participating in the overall retrospective cohort study completed

the positive predictive value study. At each of these six healthcare systems, a stratified random sample of cases with ICD-9-CM codes in the year 2003 was selected for review to estimate the positive predictive value of ICD-9-CM codes for infectious diseases. Charts were stratified by healthcare facility, by disease and by matching status (i.e., whether it was reported to the NC State Health Department) and up to 5 charts were selected per strata, but at least 20% of charts were reviewed in each strata.

Trained hospital-based public health epidemiologists (PHE) at each facility reviewed these charts for their concordance with published CDC case classification criteria for surveillance purposes [48]. Each selected patient chart was classified as either a true reportable case (i.e., confirmed, suspect, or probable) or not a case based on specified laboratory, clinical and/or epidemiological case definition criteria. Unadjusted disease-specific positive predictive values (PPV) were calculated based on the number of ICD-9-CM coded patients that were true cases by CDC criteria divided by the total number of ICD-9-CM coded patient charts that were reviewed. For each strata, empirical continuity corrections were used when no true cases were found upon review [75] and disease-specific data were aggregated across matching strata and healthcare facilities with sample proportion weighting. Adjusted completeness proportions and 95% uncertainty intervals (UI) were calculated using semi-Bayesian hierarchical regression analysis [77] as recommended to reduce the mean squared error when an ensemble of measures are estimated [71].

This semi-Bayesian hierarchical regression analysis utilizes prior covariates data that help to explain the mean of the ensemble of estimates as well as a specified prior variance (tau^2) of the distribution. Traditional maximum likelihood estimates (i.e., unadjusted estimates as presented here) can be viewed as a special case of semi-Bayesian analysis in which the prior variance is infinite. By specifying even a moderately informative prior variance such as a tau^2 indicating that 95% of all completeness proportions lie between 0.4% and 90%, an appreciable reduction in the overall mean squared error can be expected with a shift in the point estimate and a narrowing of the 95% uncertainty interval for each PPV, with the relative degree of narrowing being greater for disease with less information.

A sensitivity analysis was conducted on the specified prior variance (tau^2) using high, medium and low tau^2 values that assumed that 95% of the PPV were within the following ranges: [0.4, 99%], [0.4, 90%], [16, 70%], respectively. Sensitivity analyses were also conducted on the inclusion or exclusion of prior covariates: whether or not the disease had a reportable laboratory result, whether or not the disease had reportable serology test results, and whether or not the disease is rare in NC (<10 reported cases statewide annually).

D. Results

A total of 670 charts were reviewed for 47 different diseases. Unadjusted and semi-Bayesian adjusted disease-specific PPVs with 95% confidence intervals (CI) and uncertainty intervals (UI), respectively are summarized in Table 13. Semi-Bayesian adjusted PPVs ranged from 20.3% to 96%. Many of the higher incident diseases in NC (e.g., pertussis, invasive group A streptococcal infection, campylobacteriosis, shigellosis, salmonellosis) and more severe (e.g., meningococcal meningitis, hemolytic uremic syndrome) had PPVs exceeding 80%, although tuberculosis was very low with a PPV and 95% UI of 28.60% (15.57-46.53%). Marked differences in the unadjusted to adjusted point estimates were noted for Rocky Mountain spotted fever (RMSF), Lyme disease, *Hemophilus influenzae* invasive disease, and acute hepatitis A; however, wide uncertainty intervals also reflect the imprecision in these estimates.

The sensitivity analysis of the tau^2 values showed that the point estimates and UI were relatively insensitive to dramatic changes in tau^2; for example, for tuberculosis with a low tau, the PPV and 95% UI was estimated as: 34% (20-51%), with a medium tau, 27% (15-45%); and with a high tau, 25% (13-42%). However, the sensitivity analyses examining the use of prior covariates (Table 14) were shown to have dramatic effects on the point estimates for diseases with sparse data (e.g., *Vibrio* infection, cholera, measles) and only produced minor changes for diseases with more data (e.g., salmonellosis, meningococcal meningitis).

Table 13. ICD-9-CM Positive Predictive Values (PPV) for CDC Communicable Disease Surveillance Case Definitions

Communicable Disease	Number Charts Re-viewed	Unadjusted PPV	Lower 95% CI	Upper 95% CI	Semi-Bayesian Adjusted PPV	Lower 95% UI	Upper 95% UI
Arboviral Encephalitis	6	99.65%	0.01%	100.00%	90.33%	4.02%	99.95%
Brucellosis	3	0.16%	0.00%	100.00%	22.73%	0.08%	99.10%
Campylobacteriosis	16	99.34%	2.65%	100.00%	90.37%	33.00%	99.44%
Cholera	1	0.23%	0.00%	100.00%	23.06%	0.08%	99.13%
Creutzfeldt-Jakob Disease	5	0.08%	0.00%	100.00%	49.18%	6.74%	92.84%
Cryptosporidiosis	13	99.61%	0.01%	100.00%	88.99%	27.52%	99.42%
Cyclosporiasis	1	0.23%	0.00%	100.00%	23.06%	0.08%	99.13%
Dengue	2	0.23%	0.00%	100.00%	25.38%	0.72%	94.13%
Diphtheria	2	0.12%	0.00%	100.00%	52.97%	0.39%	99.69%
E. coli O157:H7	1	99.77%	0.00%	100.00%	88.11%	24.84%	99.40%
Foodborne Disease, Staphy-lococcal	1	99.77%	0.00%	100.00%	96.02%	6.45%	99.99%
Granulocytic Ehrlichiosis	3	0.06%	0.00%	97.60%	20.29%	0.61%	91.31%
Hantavirus	1	0.23%	0.00%	100.00%	25.77%	0.72%	94.31%
Hemolytic Uremic Syndrome	24	92.57%	67.30%	98.69%	84.62%	55.60%	96.03%
Hepatitis A, acute	62	7.79%	0.00%	99.99%	85.37%	22.23%	99.17%
Hemophilus influenzae, inva-sive disease	59	6.50%	0.00%	100.00%	86.67%	23.22%	99.29%
Legionellosis	14	99.43%	0.35%	100.00%	89.65%	30.01%	99.43%
Leptospirosis	5	0.16%	0.00%	100.00%	22.73%	0.08%	99.10%
Listeriosis	15	99.75%	0.12%	100.00%	89.54%	29.14%	99.44%
Lyme Disease	46	5.62%	0.00%	100.00%	87.10%	23.58%	99.33%
Malaria	14	99.23%	0.00%	100.00%	88.44%	25.93%	99.40%
Measles	3	99.31%	0.00%	100.00%	28.32%	0.86%	94.76%
Meningococcal meningitis	31	98.19%	56.67%	99.96%	93.36%	55.41%	99.38%

Communicable Disease	Number Charts Reviewed	Unadjusted PPV	Lower 95% CI	Upper 95% CI	Semi-Bayesian Adjusted PPV	Lower 95% UI	Upper 95% UI
Monocytic Ehrlichosis	1	99.77%	0.00%	100.00%	89.56%	3.29%	99.95%
Mumps	9	99.54%	0.00%	100.00%	28.27%	0.85%	94.77%
Plague	3	0.14%	0.00%	100.00%	22.87%	0.08%	99.12%
Pneumococcal meningitis	26	99.40%	46.16%	100.00%	93.08%	47.18%	99.51%
Poliovirus	2	0.23%	0.00%	100.00%	22.71%	0.08%	99.09%
Psittacosis	4	0.23%	0.00%	100.00%	25.38%	0.72%	94.13%
Q fever	4	50.00%	12.35%	87.65%	40.71%	9.48%	81.82%
Rabies, human	1	0.23%	0.00%	100.00%	23.06%	0.08%	99.13%
Rocky Mountain spotted fever	46	21.13%	0.06%	99.20%	83.32%	3.96%	99.84%
Rubella Congenital Syndrome	2	0.23%	0.00%	100.00%	25.77%	0.72%	94.31%
Rubella	7	0.10%	0.00%	100.00%	24.99%	0.71%	93.97%
Salmonellosis	64	99.52%	83.48%	99.99%	95.64%	66.04%	99.60%
Shigellosis	37	99.62%	17.67%	100.00%	91.75%	38.55%	99.50%
Smallpox	3	0.12%	0.00%	100.00%	21.84%	0.08%	99.01%
Streptococcal Infection, group A, invasive	12	99.44%	0.00%	100.00%	88.79%	26.98%	99.41%
Tetanus	3	0.23%	0.00%	100.00%	49.38%	6.79%	92.89%
Toxic Shock Syndrome	25	43.32%	13.56%	78.82%	45.11%	17.53%	76.06%
Trichinosis	4	0.16%	0.00%	100.00%	23.03%	0.08%	99.13%
Tuberculosis	73	23.39%	12.10%	40.37%	28.60%	15.57%	46.53%
Tularemia	2	0.23%	0.00%	100.00%	23.06%	0.08%	99.13%
Typhoid, acute	1	99.77%	0.00%	100.00%	50.62%	7.11%	93.21%
Vaccinia	3	0.23%	0.00%	100.00%	22.71%	0.08%	99.09%
Vibrio infection, other	1	99.77%	0.00%	100.00%	23.95%	0.08%	99.17%
Whooping Cough (Pertussis)	9	99.63%	0.00%	100.00%	90.09%	3.78%	99.95%

Table 14. Sensitivity Analysis for Prior Covariates on Disease-Specific Positive Predictive Values (95% UI)

Communicable Disease	All Prior Covariates	No Prior Covariates	Lab Covariate Alone	Serology Covariate Alone	Rare Disease Covariate Alone
Arboviral Encephalitis	0.9 (0.04, 1)	0.78 (0.18, 0.98)	0.79 (0.17, 0.99)	0.45 (0.02, 0.97)	0.89 (0.28, 0.99)
Brucellosis	0.23 (0, 0.99)	0.75 (0.15, 0.98)	0.76 (0.14, 0.98)	0.49 (0.07, 0.93)	0.49 (0.07, 0.93)
Campylobacteriosis	0.9 (0.33, 0.99)	0.82 (0.22, 0.99)	0.82 (0.22, 0.99)	0.6 (0.11, 0.95)	0.9 (0.34, 0.99)
Cholera	0.23 (0, 0.99)	0.76 (0.15, 0.98)	0.77 (0.14, 0.98)	0.49 (0.07, 0.93)	0.49 (0.07, 0.93)
Creutzfeldt-Jakob Disease	0.49 (0.07, 0.93)	0.75 (0.15, 0.98)	0.49 (0.07, 0.93)	0.49 (0.07, 0.93)	0.49 (0.07, 0.93)
Cryptosporidiosis	0.89 (0.28, 0.99)	0.78 (0.18, 0.98)	0.79 (0.17, 0.99)	0.54 (0.08, 0.94)	0.89 (0.28, 0.99)
Cyclosporiasis	0.23 (0, 0.99)	0.76 (0.15, 0.98)	0.77 (0.14, 0.98)	0.49 (0.07, 0.93)	0.49 (0.07, 0.93)
Dengue	0.25 (0.01, 0.94)	0.75 (0.15, 0.98)	0.76 (0.14, 0.98)	0.4 (0.02, 0.96)	0.49 (0.07, 0.93)
Diptheria	0.53 (0, 1)	0.76 (0.15, 0.98)	0.49 (0.07, 0.93)	0.4 (0.02, 0.96)	0.49 (0.07, 0.93)
E.coli O157:H7	0.88 (0.25, 0.99)	0.77 (0.16, 0.98)	0.78 (0.15, 0.99)	0.51 (0.07, 0.93)	0.88 (0.26, 0.99)
Foodborne Disease, Staphylococcal	0.96 (0.06, 1)	0.77 (0.16, 0.98)	0.51 (0.07, 0.93)	0.51 (0.07, 0.93)	0.88 (0.26, 0.99)
Granulocytic Ehrlichiosis	0.2 (0.01, 0.91)	0.67 (0.11, 0.97)	0.68 (0.11, 0.97)	0.33 (0.01, 0.94)	0.4 (0.05, 0.9)
Hantavirus	0.26 (0.01, 0.94)	0.76 (0.15, 0.98)	0.77 (0.14, 0.98)	0.41 (0.02, 0.96)	0.49 (0.07, 0.93)
Hemophilus influenzae, invasive disease	0.87 (0.23, 0.99)	0.74 (0.15, 0.98)	0.75 (0.14, 0.98)	0.48 (0.07, 0.92)	0.87 (0.24, 0.99)
Hemolytic Uremic Syndrome	0.85 (0.56, 0.96)	0.89 (0.63, 0.97)	0.85 (0.56, 0.96)	0.85 (0.56, 0.96)	0.85 (0.56, 0.96)
Hepatitis A, acute	0.85 (0.22, 0.99)	0.73 (0.14, 0.98)	0.74 (0.14, 0.98)	0.47 (0.07, 0.92)	0.86 (0.23, 0.99)
Legionellosis	0.9 (0.3, 0.99)	0.8 (0.2, 0.98)	0.81 (0.19, 0.99)	0.57 (0.1, 0.94)	0.9 (0.31, 0.99)
Leptospirosis	0.23 (0, 0.99)	0.75 (0.15, 0.98)	0.76 (0.14, 0.98)	0.49 (0.07, 0.93)	0.49 (0.07, 0.93)
Listeriosis	0.9 (0.29, 0.99)	0.8 (0.19, 0.98)	0.8 (0.18, 0.99)	0.56 (0.09, 0.94)	0.9 (0.3, 0.99)
Lyme Disease	0.87 (0.24, 0.99)	0.75 (0.15, 0.98)	0.76 (0.14, 0.98)	0.49 (0.07, 0.93)	0.87 (0.24, 0.99)
Malaria	0.88 (0.26, 0.99)	0.77 (0.17, 0.98)	0.78 (0.16, 0.99)	0.52 (0.08, 0.93)	0.89 (0.27, 0.99)
Measles	0.28 (0.01, 0.95)	0.77 (0.17, 0.98)	0.78 (0.16, 0.99)	0.43 (0.02, 0.97)	0.52 (0.08, 0.94)
Meningococcal meningitis	0.93 (0.55, 0.99)	0.89 (0.45, 0.99)	0.89 (0.45, 0.99)	0.79 (0.3, 0.97)	0.93 (0.56, 0.99)
Monocytic Ehrlichosis	0.9 (0.03, 1)	0.77 (0.16, 0.98)	0.78 (0.15, 0.99)	0.42 (0.02, 0.97)	0.88 (0.26, 0.99)
Mumps	0.28 (0.01, 0.95)	0.77 (0.17, 0.98)	0.78 (0.16, 0.99)	0.43 (0.02, 0.97)	0.52 (0.08, 0.94)
Plague	0.23 (0, 0.99)	0.75 (0.15, 0.98)	0.76 (0.14, 0.98)	0.49 (0.07, 0.93)	0.49 (0.07, 0.93)
Pneumococcal meningitis	0.93 (0.47, 1)	0.87 (0.36, 0.99)	0.88 (0.35, 0.99)	0.73 (0.21, 0.97)	0.93 (0.48, 1)
Poliovirus	0.23 (0, 0.99)	0.75 (0.15, 0.98)	0.76 (0.14, 0.98)	0.49 (0.07, 0.93)	0.49 (0.07, 0.93)
Psittacosis	0.25 (0.01, 0.94)	0.75 (0.15, 0.98)	0.76 (0.14, 0.98)	0.4 (0.02, 0.96)	0.49 (0.07, 0.93)

Communicable Disease	All Prior Covariates	No Prior Covariates	Lab Covariate Alone	Serology Covariate Alone	Rare Disease Covariate Alone
Q fever	0.41 (0.09, 0.82)	0.6 (0.23, 0.89)	0.61 (0.23, 0.89)	0.47 (0.12, 0.85)	0.5 (0.17, 0.83)
Rabies, human	0.23 (0, 0.99)	0.76 (0.15, 0.98)	0.77 (0.14, 0.98)	0.49 (0.07, 0.93)	0.49 (0.07, 0.93)
Rocky Mountain spotted fever	0.83 (0.04, 1)	0.69 (0.14, 0.97)	0.7 (0.14, 0.97)	0.38 (0.02, 0.94)	0.82 (0.22, 0.99)
Rubella Congenital Syndrome	0.26 (0.01, 0.94)	0.76 (0.15, 0.98)	0.77 (0.14, 0.98)	0.41 (0.02, 0.96)	0.49 (0.07, 0.93)
Rubella	0.25 (0.01, 0.94)	0.75 (0.15, 0.98)	0.76 (0.14, 0.98)	0.39 (0.02, 0.96)	0.48 (0.07, 0.93)
Salmonellosis	0.96 (0.66, 1)	0.93 (0.56, 0.99)	0.93 (0.56, 0.99)	0.85 (0.41, 0.98)	0.96 (0.67, 1)
Shigellosis	0.92 (0.39, 0.99)	0.84 (0.27, 0.99)	0.85 (0.27, 0.99)	0.66 (0.14, 0.96)	0.92 (0.39, 0.99)
Smallpox	0.22 (0, 0.99)	0.74 (0.14, 0.98)	0.75 (0.14, 0.98)	0.47 (0.06, 0.92)	0.47 (0.06, 0.92)
Streptococcal Infection, group A, invasive	0.89 (0.27, 0.99)	0.78 (0.17, 0.98)	0.79 (0.17, 0.99)	0.53 (0.08, 0.94)	0.89 (0.28, 0.99)
Tetanus	0.49 (0.07, 0.93)	0.76 (0.15, 0.98)	0.49 (0.07, 0.93)	0.49 (0.07, 0.93)	0.49 (0.07, 0.93)
Toxic Shock Syndrome	0.45 (0.18, 0.76)	0.53 (0.22, 0.82)	0.45 (0.18, 0.76)	0.45 (0.18, 0.76)	0.45 (0.18, 0.76)
Trichinosis	0.23 (0, 0.99)	0.76 (0.15, 0.98)	0.77 (0.14, 0.98)	0.49 (0.07, 0.93)	0.49 (0.07, 0.93)
Tuberculosis	0.29 (0.16, 0.47)	0.27 (0.15, 0.45)	0.27 (0.15, 0.45)	0.25 (0.14, 0.42)	0.29 (0.16, 0.47)
Tularemia	0.23 (0, 0.99)	0.76 (0.15, 0.98)	0.77 (0.14, 0.98)	0.49 (0.07, 0.93)	0.49 (0.07, 0.93)
Typhoid, acute	0.51 (0.07, 0.93)	0.77 (0.16, 0.98)	0.51 (0.07, 0.93)	0.51 (0.07, 0.93)	0.51 (0.07, 0.93)
Vaccinia	0.23 (0, 0.99)	0.75 (0.15, 0.98)	0.76 (0.14, 0.98)	0.49 (0.07, 0.93)	0.49 (0.07, 0.93)
Vibrio infection, other	0.24 (0, 0.99)	0.77 (0.16, 0.98)	0.78 (0.15, 0.99)	0.51 (0.07, 0.93)	0.51 (0.07, 0.93)
Whooping Cough (Pertussis)	0.9 (0.04, 1)	0.78 (0.17, 0.98)	0.79 (0.17, 0.99)	0.44 (0.02, 0.97)	0.89 (0.28, 0.99)

E.   Discussion

We found that for many diseases of particular interest to the public health community the positive predictive values of the ICD-9-CM codes were relatively high with a notable exception of tuberculosis. Tuberculosis posed a particular problem with assignment of ICD-9-CM codes because of the difficulties with clinical diagnoses, that is, Mycobacteria are slow-growing organisms, patients can be latently infected without having active disease, and patients are often started on empiric therapy until active tuberculosis can be ruled out because of the public health impact of a communicable airborne disease. Other diseases with low positive predictive values estimates included unlikely or improbable diseases such as human rabies, hantavirus, poliovirus, smallpox, plague; diseases which are relatively rare, such as measles, mumps, rubella, Creutzfeldt-Jakob disease, and diseases which have complex surveillance case definitions, such as toxic shock syndrome. Hemolytic uremic syndrome also has a complex surveillance case definition, but is almost always associated with isolation of *E. coli* O157:H7, which may explain its higher PPV than toxic shock syndrome.

We believe that the semi-Bayesian adjusted estimates offer improved overall accuracy and precision for our ensemble of PPV estimates. Based on the results of our sensitivity analysis for the prior covariates, we elected to use the model that included all prior covariates as it allowed for more conservative estimates with a wider range of values. In addition, we chose a prior variance (tau^2) that conservatively reduced the overall mean's likely 95% confidence interval from 0-100% to 0.4-90%. The effect of semi-Bayesian analysis methods can be seen in the change in PPVs for RMSF, Lyme disease, *H. influenzae* invasive disease, and acute hepatitis A. All of these diseases had relatively low positive predictive values (<25%) that after semi-Bayesian adjustment increased to over 80%, as they became shrunk towards the mean of their prior covariates (i.e., they are all not rare diseases and have laboratory results). However, the imprecision of these estimates is still reflected in their wide uncertainty intervals. Furthermore, these diseases share similar properties with other low PPV diseases in that their case definitions are complex and/or clinical diagnoses are difficult to make. Both

RMSF and Lyme disease require acute and convalescent serology for confirmation of disease to meet the confirmed case definition. Invasive disease, including pneumonia, with *H. influenzae* requires isolation of the bacteria from a sterile body site and positive hepatitis A serology results indicating vaccination or a previous infection can be misinterpreted as an acute infection.

Despite the use of trained medical coders at healthcare systems who review providers' documentation to assign the ICD-9-CM diagnosis codes following the patient's discharge or outpatient visit, these codes are not assigned without errors. Occasionally, we found ICD-9-CM codes that were mistakenly assigned for a similar sounding disease; for example, a patient with a head ultrasound abbreviated as HUS, was coded as hemolytic uremic syndrome or a patient with pleural plaques noted on a chest radiograph was assigned a diagnosis code for plague. Sometimes similar infectious diseases were mistakenly assigned; for example, hepatitis C instead of hepatitis A or monocytic ehrlichiosis instead of granulocytic ehrlichiosis. Finally, there were a limited number of cases with no data in the medical record to support the diagnostic code. However, these situations occurred most often with rare or difficult to diagnose diseases.

This study may have been limited by the availability of data on which to evaluate each case's concordance with CDC case definitions. While the CDC case definitions are standardized and utilized nationwide for communicable disease surveillance, some of the case definitions include complex criteria that are difficult to apply objectively to clinical cases. Each PHE was trained to apply these case definitions as objectively as possible during the chart review in the validation study, but misclassification of patients could have occurred due to incomplete clinical data in the patient's medical record or the interpretation of a complex case definition criteria. However, a senior medical epidemiologist at the NC DHHS was available to provide assistance with interpretation of complex case definition criteria and application to clinical or laboratory data.

In order to truly understand the utility of ICD-9-CM codes for infectious disease surveillance, additional comprehensive studies are warranted to estimate the sensitivity of ICD-9-CM codes. While this study has provided the most comprehensive assessment of positive predictive values for ICD-9-CM for infectious disease surveillance to date, we were not able to estimate the sensitivity of ICD-9-

CM codes due to the cost and difficulties in identifying an appropriate gold standard. A previous study conducted by Watkins et al. which showed low ICD-9-CM sensitivity used laboratory records as the "gold" standard for five laboratory reportable diseases; however, this method is only appropriate for those diseases with straightforward laboratory findings. Ideally, a complete medical record review would serve as a gold standard, but would be both extremely costly and time-consuming and would be very inefficient for most of the infectious diseases with relatively low incidence rates in the general population. With estimates of both positive predictive values and sensitivity of ICD-9-CM codes, not only can the utility of these codes be completely described but an adjustment of ICD-9-CM based studies can be conducted using Bayes Theorem (Appendix 3).

The standardized designation of ICD-9-CM codes to capture a patient's clinical diagnosis make them attractive data elements for automated, electronic disease surveillance and as new case definitions are developed to be compatible with automated, electronic public health surveillance, the utility of ICD-9-CM codes should be carefully considered. Based on our findings, we believe that ICD-9-CM codes for communicable diseases have high enough positive predictive values to be useful for diseases which are relatively common and have simple case definitions and clinical diagnoses. ICD-9-CM codes are inefficient for studying rare diseases (e.g., brucellosis, Q fever) or to conduct surveillance for unlikely diseases (e.g., smallpox, anthrax) because of the high number of false positive cases.

VI.   Chapter 6: Conclusions

A.   Recapitulation of Specific Aims

Aim 1: Determine the positive predictive value (PPV) of diagnostic codes for communicable disease case ascertainment and surveillance. That is, given that a patient is assigned a diagnostic code for a communicable disease, the probability that the patient meets the communicable disease case definition will be determined.

Conclusions: We found that for many diseases of particular interest to the public health community the positive predictive values of the ICD-9-CM codes were relatively high with the notable exception of tuberculosis.   Other diseases with low positive predictive values estimates included unlikely or improbable diseases such as human rabies, hantavirus, poliovirus, smallpox, plague; diseases which are relatively rare, such as measles, mumps, rubella, Creutzfeldt-Jakob disease, and diseases which have complex surveillance case definitions, such as toxic shock syndrome.

Aim 2: Describe the disease-specific completeness of state-required communicable disease reporting, overall state-required communicable disease reporting over a 10 year time period, and overall state-required communicable disease reporting for different healthcare systems.

Conclusions: Disease-specific reporting completeness proportions were estimated to be very low and varied greatly based on disease. One clear pattern that emerged in our findings was that diseases with fewer clinical criteria and laboratory-based case definitions tended to have higher reporting rates. The overall disease reporting completeness proportions for eight different healthcare systems ranged

widely from 2-30% and the general trend of the yearly reporting completeness proportions suggests that disease reporting has improved over time yet remains very low.

Aim 3: Utilize hierarchical Bayesian analysis techniques to provide more precise estimates of disease-specific reporting completeness and positive predictive values of ICD-9-CM codes.

Conclusions: We believe that the semi-Bayesian adjusted estimates offer improved overall accuracy and precision for our ensemble of disease reporting completeness proportions and PPV estimates. We did note several dramatic shifts in the reporting completeness proportions and PPVs after semi-Bayesian adjustments. These shifts reflected both the imprecision in each disease's measured estimates and the shrinkage of their proportions to others in the same prior covariate group. This finding reinforces the importance of careful specification of prior covariates as well as judicious examination and interpretation of unadjusted and semi-Bayesian adjusted estimates along with their precision.

B. Recommendations

In order to fully understand the utility of ICD-9-CM codes for infectious disease surveillance, additional comprehensive studies are warranted to estimate the sensitivity of ICD-9-CM codes. While this study has provided the most comprehensive assessment of positive predictive values for ICD-9-CM for infectious disease surveillance to date, we were not able to estimate the sensitivity of ICD-9-CM codes due to the cost and difficulties in identifying an appropriate gold standard. When estimates of both positive predictive values and sensitivity of ICD-9-CM codes are available, not only can the utility of these codes be completely described but an adjustment of ICD-9-CM based studies can be conducted using Bayes Theorem.

However, based on our findings, we believe that ICD-9-CM codes for communicable diseases have high enough positive predictive values to be useful for studying diseases which are relatively common and have simple case definitions and clinical diagnoses. ICD-9-CM codes are inefficient for

studying rare diseases (e.g., brucellosis, Q fever) or to conduct surveillance for unlikely diseases (e.g., smallpox, anthrax) because of the high number of false positive cases.

We found disease reporting to be very low overall even for diseases that require immediate public health intervention. Complete communicable disease reporting is critical to the success of the public health surveillance system, and physicians and laboratories should be provided with ongoing education on the importance of public health surveillance. The benefit of programs like hospital-based PHEs is that they can be directly involved in developing and delivering this education to physicians and laboratorians in their healthcare systems in grand round formats, inservices, and direct interactions.

One clear pattern that emerged in our findings was that diseases with fewer clinical criteria and laboratory-based case definitions tended to have higher reporting rates. We also found that the requirement for laboratories to report diseases with positive laboratory findings improved overall disease reporting though it still remained low. Therefore, the impact of the complexity of case definitions on the reporting completeness should be a consideration in surveillance system development and maintenance.

Future studies may include an investigation on predictors of reporting or timeliness of reporting related to the patient interaction (e.g., number of visits, length of stay, and location of visit) and disease characteristics (e.g., mode of transmission, whether the disease has laboratory test results). Additional studies are also warranted to investigate what healthcare system factors predict higher reporting rates among the healthcare systems as we did not find that assigning responsibility to another entity (i.e., PHE, infection preventionist) had a statistically significant effect on reporting. Results from these additional studies may help in the improvement of current surveillance strategies or the development of surveillance innovations.

Finally, both state health departments and healthcare systems should consider investing in technology for automating both disease reporting and surveillance data collection. Automated disease reporting could be achieved by standardized queries directly from the electronic health records for

key laboratory results and for simplified or proxy clinical case definitions using ICD-9-CM diagnosis codes or free-text admission diagnoses. Upon recognition of these potential case-patients, automating surveillance data collection directly from electronic health records to populate data fields for basic patient demographics and laboratory results could also significantly reduce administrative time for physicians and health department officials and expedite disease investigations. Using the electronic health record for automated case-finding and data collection would transition our current public health surveillance system from passive to active and thereby overcome the major barriers to complete, accurate and timely communicable disease reporting and surveillance.

VII.   Appendices

Appendix 1: ICD-9-CM code list

Anthrax	022	ANTHRAX
Anthrax	022.0	CUTANEOUS ANTHRAX
Anthrax	022.1	PULM ANTHRAX
Anthrax	022.2	GASTROINTESTINAL ANTHRAX
Anthrax	022.3	ANTHRAX SEPTICEMIA
Anthrax	022.8	OTH SPEC MANIFESTATIONS OF ANTHRAX
Anthrax	022.9	ANTHRAX, UNSPEC
Anthrax	484.5	PNEUMONIA IN ANTHRAX
Botulism	005.1	BOTULISM
Brucellosis	023	BRUCELLOSIS
Brucellosis	023.0	BRUCELLA MELITENSIS
Brucellosis	023.1	BRUCELLA ABORTUS
Brucellosis	023.2	BRUCELLA SUIS
Brucellosis	023.3	BRUCELLA CANIS
Brucellosis	023.8	OTH BRUCELLOSIS
Brucellosis	023.9	BRUCELLOSIS, UNSPEC
Campylobacter	008.43	INTESTINAL INFEC DUE TO CAMPYLOBACTER
Chancroid	099.0	CHANCROID
Cholera	001.0	CHOLERA DUE TO VIBRIO CHOLERAE
Cholera	001.1	CHOLERA DUE TO VIBRIO CHOLERAE EL TOR
Cryptosporidiosis	007.4	CRYPTOSPORIDIOSIS
Cyclosporiasis	007.5	CYCLOSPORIASIS
Dengue	061	DENGUE
Dengue	065.4	HEMMORRHAGIC FEVER CAUSED BY DENGUE VIRUS
Diphtheria	032.0	FAUCIAL DIPHTHERIA
Diphtheria	032.1	NASOPHARYNGEAL DIPHTHERIA
Diphtheria	032.2	ANTERIOR NASAL DIPHTHERIA
Diphtheria	032.3	LARYNGEAL DIPHTHERIA
E.coli 017:H7	008.04	INTESTINAL INFEC DUE TO ENTEROHEMORRHAGIC E. COLI
Ehrlichiosis, granulocytic	082.40	EHRLICHIOSIS
Ehrlichiosis, granulocytic	082.49	OTH EHRLICHIOSIS
Ehrlichiosis, monocytic	082.41	EHRLICHIOSIS CHAFEENSIS (E CHAFEENSIS)

Encephalitis, Arboviral, CAL	062.5	CALIFORNIA VIRUS ENCEPHALITIS
Encephalitis, Arboviral, EEE	062.2	EASTERN EQUINE ENCEPHALITIS
Encephalitis, Arboviral, WNV	066.4	WEST NILE FEVER
Encephalitis, Arboviral, WNV	066.40	WEST NILE FEVER, UNSPECIFIED
Encephalitis, Arboviral, WNV	066.41	WEST NILE FEVER WITH ENCEPHALITIS
Encephalitis, Arboviral, WNV	066.42	WEST NILE FEVER WITH OTHER NEUROLOGIC MANIFESTATION
Encephalitis, Arboviral, WNV	066.49	WEST NILE FEVER WITH OTHER COMPLICATIONS
Foodborne Disease: C. perfringens	005.2	FOOD POISONING DUE TO CLOSTRIDIUM PERFRINGENS (C. WELCHII)
Foodborne Disease: Staphylococcal	005.0	STAPHYLOCOCCAL FOOD POISONING
Hantavirus	079.81	HANTAVIRUS
Hemolytic Uremic Syndrome	283.11	HEMOLYTIC-UREMIC SYNDROME
Hemophilus Influenzae, Invasive Disease	038.41	SEPTICEMIA DUE TO HEMOPHILUS INFLUENZAE (H. INFLUENZAE)
Hemophilus Influenzae, Invasive Disease	320.0	HEMOPHILUS MENINGITIS
Hemophilus Influenzae, Invasive Disease	482.2	PNEUMONIA DUE TO HEMOPHILUS INFLUENZAE (H. INFLUENZAE)
Hepatitis A	070	VIRAL HEP A WITH HEPATIC COMA
Hepatitis A	070.1	VIRAL HEP A NO HEPATIC COMA
Legionellosis	482.84	PNEUMONIA DUE TO LEGIONNAIRES' DISEASE
Leptospirosis	100	LEPTOSPIROSIS
Leptospirosis	100.0	LEPTOSPIROSIS ICTEROHEMORRHAGICA
Leptospirosis	100.8	OTH SPEC LEPTOSPIRAL INFEC
Leptospirosis	100.81	LEPTOSPIRAL MENINGITIS (ASEPTIC)
Leptospirosis	100.89	OTH SPEC LEPTOSPIRAL INFEC
Leptospirosis	100.9	LEPTOSPIROSIS, UNSPEC
Listeriosis	027.0	LISTERIOSIS
Lyme Disease	088.81	LYME DISEASE
Malaria	084	MALARIA
Malaria	084.0	FALCIPARUM MALARIA (MALIGNANT TERTIAN)
Malaria	084.1	VIVAX MALARIA (BENIGN TERTIAN)
Malaria	084.2	QUARTAN MALARIA
Malaria	084.3	OVALE MALARIA
Malaria	084.4	OTH MALARIA
Malaria	084.5	MIXED MALARIA
Malaria	084.6	MALARIA, UNSPEC

Malaria	084.7	INDUCED MALARIA
Malaria	084.8	BLACKWATER FEVER
Malaria	084.9	OTH PERNICIOUS COMPLICATIONS OF MALARIA
Measles (rubeola)	055	MEASLES
Measles (rubeola)	055.0	POSTMEASLES ENCEPHALITIS
Measles (rubeola)	055.1	POSTMEASLES PNEUMONIA
Measles (rubeola)	055.2	POSTMEASLES OTITIS MEDIA
Measles (rubeola)	055.7	MEASLES WITH OTH SPEC COMPLICATIONS
Measles (rubeola)	055.71	MEASLES KERATOCONJUNCTIVITIS
Measles (rubeola)	055.79	MEASLES WITH OTH SPEC COMPLICATIONS
Measles (rubeola)	055.8	MEASLES WITH UNSPEC COMPLICATION
Measles (rubeola)	055.9	MEASLES NO COMPLICATION
Meningitis, Pneumococcal meningitis	320.1	PNEUMOCOCCAL MENINGITIS
Meningococcal Disease	036	MENINGOCOCCAL INFEC
Meningococcal Disease	036.0	MENINGOCOCCAL MENINGITIS
Meningococcal Disease	036.1	MENINGOCOCCAL ENCEPHALITIS
Meningococcal Disease	036.2	MENINGOCOCCEMIA
Meningococcal Disease	036.3	WATERHOUSE-FRIDERICHSEN SYNDROME, MENINGOCOCCAL
Meningococcal Disease	036.4	MENINGOCOCCAL CARDITIS
Meningococcal Disease	036.40	MENINGOCOCCAL CARDITIS, UNSPEC
Meningococcal Disease	036.41	MENINGOCOCCAL PERICARDITIS
Meningococcal Disease	036.42	MENINGOCOCCAL ENDOCARDITIS
Meningococcal Disease	036.43	MENINGOCOCCAL MYOCARDITIS
Meningococcal Disease	036.8	OTH SPEC MENINGOCOCCAL INFEC
Meningococcal Disease	036.81	MENINGOCOCCAL OPTIC NEURITIS
Meningococcal Disease	036.82	MENINGOCOCCAL ARTHROPATHY
Meningococcal Disease	036.89	OTH SPEC MENINGOCOCCAL INFEC
Mumps	072	MUMPS
Mumps	072.0	MUMPS ORCHITIS
Mumps	072.1	MUMPS MENINGITIS
Mumps	072.2	MUMPS ENCEPHALITIS
Mumps	072.3	MUMPS PANCREATITIS
Mumps	072.7	MUMPS WITH OTH SPEC COMPLICATIONS
Mumps	072.71	MUMPS HEPATITIS
Mumps	072.72	MUMPS POLYNEUROPATHY

Mumps	072.79	MUMPS WITH OTH SPEC COMPLICATIONS
Mumps	072.8	MUMPS WITH UNSPEC COMPLICATION
Mumps	072.9	MUMPS NO COMPLICATION
Pelvic Inflammatory Disease	614.9	UNSPECIFIED INFLAMMATORY DISEASE OF FEMALE PELVIC ORGANS AND TISSUES
Plague	020	PLAGUE
Plague	020.0	BUBONIC PLAGUE
Plague	020.1	CELLULOCUTANEOUS PLAGUE
Plague	020.2	SEPTICEMIC PLAGUE
Plague	020.3	PRIM PNEUMONIC PLAGUE
Plague	020.4	SECONDARY PNEUMONIC PLAGUE
Plague	020.5	PNEUMONIC PLAGUE, UNSPEC
Plague	020.8	OTH SPEC TYPES OF PLAGUE
Plague	020.9	PLAGUE, UNSPEC
Poliomyelitis, Paralytic	045	ACUTE POLIOMYELITIS
Poliomyelitis, Paralytic	045.0	ACUTE PARALYTIC POLIOMYELITIS SPEC AS BULBAR
Poliomyelitis, Paralytic	045.00	ACUTE PARALYTIC POLIOMYELITIS SPEC AS BULBAR, UNSPEC OF POLIOVIRUS
Poliomyelitis, Paralytic	045.01	ACUTE PARALYTIC POLIOMYELITIS SPEC AS BULBAR, POLIOVIRUS TYPE I
Poliomyelitis, Paralytic	045.02	ACUTE PARALYTIC POLIOMYELITIS SPEC AS BULBAR, POLIOVIRUS TYPE II
Poliomyelitis, Paralytic	045.03	ACUTE PARALYTIC POLIOMYELITIS SPEC AS BULBAR, POLIOVIRUS TYPE III
Poliomyelitis, Paralytic	045.1	ACUTE POLIOMYELITIS WITH OTH PARALYSIS
Poliomyelitis, Paralytic	045.10	ACUTE POLIOMYELITIS WITH OTH PARALYSIS, UNSPEC OF POLIOVIRUS
Poliomyelitis, Paralytic	045.11	ACUTE POLIOMYELITIS WITH OTH PARALYSIS, POLIOVIRUS TYPE I
Poliomyelitis, Paralytic	045.12	ACUTE POLIOMYELITIS WITH OTH PARALYSIS, POLIOVIRUS TYPE II
Poliomyelitis, Paralytic	045.13	ACUTE POLIOMYELITIS WITH OTH PARALYSIS, POLIOVIRUS TYPE III
Psittacosis	073	ORNITHOSIS
Psittacosis	073.0	ORNITHOSIS WITH PNEUMONIA
Psittacosis	073.7	ORNITHOSIS WITH OTH SPEC COMPLICATIONS
Psittacosis	073.8	ORNITHOSIS WITH UNSPEC COMPLICATION
Psittacosis	073.9	ORNITHOSIS, UNSPEC
Q Fever	083.0	Q FEVER
Rabies, Human	071	RABIES
RMSF	082.0	SPOTTED FEVERS
Rubella	056	RUBELLA
Rubella	056.0	RUBELLA WITH NEUROLOGICAL COMPLICATIONS
Rubella	056.00	RUBELLA WITH UNSPEC NEUROLOGICAL COMPLICATION

Rubella	056.01	ENCEPHALOMYELITIS DUE TO RUBELLA
Rubella	056.09	RUBELLA WITH OTH NEUROLOGICAL COMPLICATIONS
Rubella	056.7	RUBELLA WITH OTH SPEC COMPLICATIONS
Rubella	056.71	ARTHRITIS DUE TO RUBELLA
Rubella	056.79	RUBELLA WITH OTH SPEC COMPLICATIONS
Rubella	056.8	RUBELLA WITH UNSPEC COMPLICATIONS
Rubella	056.9	RUBELLA NO COMPLICATION
Rubella Congenital Syndrome	771.0	CONGENITAL RUBELLA
Salmonellosis	003	OTH SALMONELLA INFEC
Salmonellosis	003.0	SALMONELLA GASTROENTERITIS
Salmonellosis	003.1	SALMONELLA SEPTICEMIA
Salmonellosis	003.2	LOCALIZED SALMONELLA INFEC
Salmonellosis	003.20	LOCALIZED SALMONELLA INFEC, UNSPEC
Salmonellosis	003.21	SALMONELLA MENINGITIS
Salmonellosis	003.22	SALMONELLA PNEUMONIA
Salmonellosis	003.23	SALMONELLA ARTHRITIS
Salmonellosis	003.24	SALMONELLA OSTEOMYELITIS
Salmonellosis	003.29	OTH LOCALIZED SALMONELLA INFEC
Salmonellosis	003.8	OTH SPEC SALMONELLA INFEC
Salmonellosis	003.9	SALMONELLA INFEC, UNSPEC
SARS (Coronavirus Infection)	480.3	PNEUMONIA DUE TO SARS-ASSOCIATED CORONAVIRUS
SARS (Coronavirus Infection)	079.82	SARS-ASSOCIATED CORONAVIRUS
Shigellosis	004	SHIGELLOSIS
Shigellosis	004.0	SHIGELLA DYSENTERIAE
Shigellosis	004.1	SHIGELLA FLEXNERI
Shigellosis	004.2	SHIGELLA BOYDII
Shigellosis	004.3	SHIGELLA SONNEI
Shigellosis	004.8	OTH SPEC SHIGELLA INFEC
Shigellosis	004.9	SHIGELLOSIS, UNSPEC
Smallpox	050	SMALLPOX
Smallpox	050.0	VARIOLA MAJOR
Smallpox	050.1	ALASTRIM: VARIOLA MINOR
Smallpox	050.2	MODIFIED SMALLPOX
Smallpox	050.9	SMALLPOX, UNSPEC
Streptococcal Infection, Invasive GAS	041.01	STREP INFEC IN OTH CONDITIONS AND OF UNSPEC SITE, STREP, GROUP A

Streptococcal Infection, Invasive GAS	038.0	STREPTOCOCCAL SEPTICEMIA
Streptococcal Infection, Invasive GAS	320.2	STREPTOCOCCAL MENINGITIS
Streptococcal Infection, Invasive GAS	482.31	GROUP A STREPTOCOCCAL PNEUMONIA
Tetanus	037	TETANUS
Toxic Shock Syndrome	040.82	TOXIC SHOCK SYNDROME
Toxic Shock Syndrome, Streptococcal	040.82	TOXIC SHOCK SYNDROME
Toxic Shock Syndrome, Streptococcal	041.01	GROUP A STREPTOCOCCUS
Transmissible Spongiform Encephalo-pathy (CJD/vCJD)	046.1	JAKOB-CREUTZFELDT DISEASE
Trichinosis	124	TRICHINOSIS
Tuberculosis	010	PRIM TB INFEC
Tuberculosis	010.0	PRIM TB COMPLEX
Tuberculosis	010.00	PRIM TB COMPLEX, UNSPEC EXAM
Tuberculosis	010.01	PRIM TB COMPLEX, BACTERIO/HISTO NOT DONE
Tuberculosis	010.02	PRIM TB COMPLEX, BACTERIO/HISTO RESULTS UNKNOWN
Tuberculosis	010.03	PRIM TB COMPLEX, BACILLI FOUND IN SPUTUM BY MICRO
Tuberculosis	010.04	PRIM TB COMPLEX, BACILLI NOT IN SPUTUM BY MICRO BUT BY BACT CX
Tuberculosis	010.05	PRIM TB COMPLEX, BACILLI NOT BY BACTERIO EXAM BUT HISTO
Tuberculosis	010.06	PRIM TB COMPLEX, BACILLI NOT BY BACTERIO/HISTO BUT OTH METHOD
Tuberculosis	010.1	PLEURISY IN PRIM PROGR TB
Tuberculosis	010.10	PLEURISY IN PRIM PROGR TB, CONFIRMATION UNSPEC
Tuberculosis	010.11	PLEURISY IN PRIM PROGR TB, BACTERIO/HISTO NOT DONE
Tuberculosis	010.12	PLEURISY IN PRIM PROGR TB, BACTERIO/HISTO RESULTS UNKNOWN
Tuberculosis	010.13	PLEURISY IN PRIM PROGR TB, BACILLI FOUND IN SPUTUM BY MICRO
Tuberculosis	010.14	PLEURISY IN PRIM PROGR TB, BACILLI NOT IN SPUTUM BY MICRO BUT BY BACT CX
Tuberculosis	010.15	PLEURISY IN PRIM PROGR TB, BACILLI NOT BY BACTERIO EXAM BUT HISTO
Tuberculosis	010.16	PLEURISY IN PRIM PROGR TB, BACILLI NOT BY BACTERIO/HISTO BUT OTH METHOD
Tuberculosis	010.8	OTH PRIM PROGR TB
Tuberculosis	010.80	OTH PRIM PROGR TB, CONFIRMATION UNSPEC
Tuberculosis	010.81	OTH PRIM PROGR TB, BACTERIO/HISTO NOT DONE
Tuberculosis	010.82	OTH PRIM PROGR TB, BACTERIO/HISTO RESULTS UNKNOWN
Tuberculosis	010.83	OTH PRIM PROGR TB, BACILLI FOUND IN SPUTUM BY MICRO
Tuberculosis	010.84	OTH PRIM PROGR TB, BACILLI NOT IN SPUTUM BY MICRO BUT BY BACT CX
Tuberculosis	010.85	OTH PRIM PROGR TB, BACILLI NOT BY BACTERIO EXAM BUT HISTO
Tuberculosis	010.86	OTH PRIM PROGR TB, BACILLI NOT BY BACTERIO/HISTO BUT OTH METHOD

Tuberculosis	010.9	PRIM TB INFEC, UNSPEC
Tuberculosis	010.90	PRIM TB INFEC, UNSPEC, CONFIRMATION UNSPEC
Tuberculosis	010.91	PRIM TB INFEC, UNSPEC, BACTERIO/HISTO NOT DONE
Tuberculosis	010.92	PRIM TB INFEC, UNSPEC, BACTERIO/HISTO RESULTS UNKNOWN
Tuberculosis	010.93	PRIM TB INFEC, UNSPEC, BACILLI FOUND IN SPUTUM BY MICRO
Tuberculosis	010.94	PRIM TB INFEC, UNSPEC, BACILLI NOT IN SPUTUM BY MICRO BUT BY BACT CX
Tuberculosis	010.95	PRIM TB INFEC, UNSPEC, BACILLI NOT BY BACTERIO EXAM BUT HISTO
Tuberculosis	010.96	PRIM TB INFEC, UNSPEC, BACILLI NOT BY BACTERIO/HISTO BUT OTH METHOD
Tuberculosis	011	PULM TB
Tuberculosis	011.0	TB OF LUNG, INFILTRATIVE
Tuberculosis	011.00	TB OF LUNG, INFILTRATIVE, CONFIRMATION UNSPEC
Tuberculosis	011.01	TB OF LUNG, INFILTRATIVE, BACTERIO/HISTO NOT DONE
Tuberculosis	011.02	TB OF LUNG, INFILTRATIVE, BACTERIO/HISTO RESULTS UNKNOWN
Tuberculosis	011.03	TB OF LUNG, INFILTRATIVE, BACILLI FOUND IN SPUTUM BY MICRO
Tuberculosis	011.04	TB OF LUNG, INFILTRATIVE, BACILLI NOT IN SPUTUM BY MICRO BUT BY BACT CX
Tuberculosis	011.05	TB OF LUNG, INFILTRATIVE, BACILLI NOT BY BACTERIO EXAM BUT HISTO
Tuberculosis	011.06	TB OF LUNG, INFILTRATIVE, BACILLI NOT BACTERIO/HISTO BUT OTH METHOD
Tuberculosis	011.1	TB OF LUNG, NODULAR
Tuberculosis	011.10	TB OF LUNG, NODULAR, UNSPEC EXAM
Tuberculosis	011.11	TB OF LUNG, NODULAR, BACTERIO/HISTO NOT DONE
Tuberculosis	011.12	TB OF LUNG, NODULAR, BACTERIO/HISTO RESULTS UNKNOWN
Tuberculosis	011.13	TB OF LUNG, NODULAR, BACILLI FOUND IN SPUTUM BY MICRO
Tuberculosis	011.14	TB OF LUNG, NODULAR, BACILLI NOT IN SPUTUM BY MICRO BUT BY BACT CX
Tuberculosis	011.15	TB OF LUNG, NODULAR, BACILLI NOT BY BACTERIO EXAM BUT HISTO
Tuberculosis	011.16	TB OF LUNG, NODULAR, BACILLI NOT BY BACTERIO/HISTO BUT OTH METHOD
Tuberculosis	011.2	TB OF LUNG WITH CAVITATION
Tuberculosis	011.20	TB OF LUNG WITH CAVITATION, UNSPEC EXAM
Tuberculosis	011.21	TB OF LUNG WITH CAVITATION, BACTERIO/HISTO NOT DONE
Tuberculosis	011.22	TB OF LUNG WITH CAVITATION, BACTERIO/HISTO RESULTS UNKNOWN
Tuberculosis	011.23	TB OF LUNG WITH CAVITATION, BACILLI FOUND IN SPUTUM BY MICRO
Tuberculosis	011.24	TB OF LUNG WITH CAVITATION, BACILLI NOT IN SPUTUM BY MICRO BUT BY BACT CX
Tuberculosis	011.25	TB OF LUNG WITH CAVITATION, BACILLI NOT BY BACTERIO EXAM BUT HISTO
Tuberculosis	011.26	TB OF LUNG WITH CAVITATION, BACILLI NOT BY BACTERIO/HISTO BUT OTH METHOD
Tuberculosis	011.3	TB OF BRONCHUS
Tuberculosis	011.30	TB OF BRONCHUS, UNSPEC EXAM

Tuberculosis	011.31	TB OF BRONCHUS, BACTERIO/HISTO NOT DONE
Tuberculosis	011.32	TB OF BRONCHUS, BACTERIO/HISTO RESULTS UNKNOWN
Tuberculosis	011.33	TB OF BRONCHUS, BACILLI FOUND IN SPUTUM BY MICRO
Tuberculosis	011.34	TB OF BRONCHUS, BACILLI NOT IN SPUTUM BY MICRO BUT FOUND IN BACT CX
Tuberculosis	011.35	TB OF BRONCHUS, BACILLI NOT BY BACTERIO EXAM BUT HISTO
Tuberculosis	011.36	TB OF BRONCHUS, BACILLI NOT BY BACTERIO/HISTO BUT OTH METHOD
Tuberculosis	011.4	TB FIBROSIS OF LUNG
Tuberculosis	011.40	TB FIBROSIS OF LUNG, UNSPEC EXAM
Tuberculosis	011.41	TB FIBROSIS OF LUNG, BACTERIO/HISTO NOT DONE
Tuberculosis	011.42	TB FIBROSIS OF LUNG, BACTERIO/HISTOUNKNOWN
Tuberculosis	011.43	TB FIBROSIS OF LUNG, BACILLI FOUND IN SPUTUM BY MICRO
Tuberculosis	011.44	TB FIBROSIS OF LUNG, BACILLI NOT IN SPUTUM BY MICRO BUT BY BACT CX
Tuberculosis	011.45	TB FIBROSIS OF LUNG, BACILLI NOT BY BACTERIO EXAM BUT HISTO
Tuberculosis	011.46	TB FIBROSIS OF LUNG, BACILLI NOT BY BACTERIO/HISTO BUT OTH METHOD
Tuberculosis	011.5	TB BRONCHIECTASIS
Tuberculosis	011.50	TB BRONCHIECTASIS, UNSPEC EXAM
Tuberculosis	011.51	TB BRONCHIECTASIS, BACTERIO/HISTO NOT DONE
Tuberculosis	011.52	TB BRONCHIECTASIS, BACTERIO/HISTO RESULTS UNKNOWN
Tuberculosis	011.53	TB BRONCHIECTASIS, BACILLI FOUND IN SPUTUM BY MICRO
Tuberculosis	011.54	TB BRONCHIECTASIS, BACILLI NOT IN SPUTUM BY MICRO BUT BY BACT CX
Tuberculosis	011.55	TB BRONCHIECTASIS, BACILLI NOT BY BACTERIO EXAM BUT HISTO
Tuberculosis	011.56	TB BRONCHIECTASIS, BACILLI NOT BY BACTERIO/HISTO BUT OTH METHOD
Tuberculosis	011.6	TB PNEUMONIA (ANY FORM)
Tuberculosis	011.60	TB PNEUMONIA (ANY FORM), UNSPEC EXAM
Tuberculosis	011.61	TB PNEUMONIA (ANY FORM), BACTERIO/HISTO NOT DONE
Tuberculosis	011.62	TB PNEUMONIA (ANY FORM), BACTERIO/HISTO RESULTS UNKNOWN
Tuberculosis	011.63	TB PNEUMONIA (ANY FORM), BACILLI FOUND IN SPUTUM BY MICRO
Tuberculosis	011.64	TB PNEUMONIA (ANY FORM), BACILLI NOT IN SPUTUM BY MICRO BUT BY BACT CX
Tuberculosis	011.65	TB PNEUMONIA (ANY FORM), BACILLI NOT BY BACTERIO EXAM BUT HISTO
Tuberculosis	011.66	TB PNEUMONIA (ANY FORM), BACILLI NOT BY BACTERIO/HISTO BUT OTH METHOD
Tuberculosis	011.7	TB PNEUMOTHORAX
Tuberculosis	011.70	TB PNEUMOTHORAX, UNSPEC EXAM
Tuberculosis	011.71	TB PNEUMOTHORAX, BACTERIO/HISTO NOT DONE
Tuberculosis	011.72	TB PNEUMOTHORAX, BACTERIO/HISTO RESULTS UNKNOWN
Tuberculosis	011.73	TB PNEUMOTHORAX, BACILLI FOUND IN SPUTUM BY MICRO

Tuberculosis	011.74	TB PNEUMOTHORAX, BACILLI NOT IN SPUTUM BY MICRO BUT BY BACT CX
Tuberculosis	011.75	TB PNEUMOTHORAX, BACILLI NOT BY BACTERIO EXAM BUT HISTO
Tuberculosis	011.76	TB PNEUMOTHORAX, BACILLI NOT BY BACTERIO/HISTO BUT OTH METHOD
Tuberculosis	011.8	OTH SPEC PULM TB
Tuberculosis	011.80	OTH SPEC PULM TB, UNSPEC CONFIRMATION
Tuberculosis	011.81	OTH SPEC PULM TB, BACTERIO/HISTO NOT DONE
Tuberculosis	011.82	OTH SPEC PULM TB, BACTERIO/HISTO RESULTS UNKNOWN
Tuberculosis	011.83	OTH SPEC PULM TB, BACILLI FOUND IN SPUTUM BY MICRO
Tuberculosis	011.84	OTH SPEC PULM TB, BACILLI NOT IN SPUTUM BY MICRO BUT BY BACT CX
Tuberculosis	011.85	OTH SPEC PULM TB, BACILLI NOT BY BACTERIO EXAM BUT HISTO
Tuberculosis	011.86	OTH SPEC PULM TB, BACILLI NOT BY BACTERIO/HISTO BUT OTH METHOD
Tuberculosis	011.9	UNSPEC PULM TB
Tuberculosis	011.90	UNSPEC PULM TB, CONFIRMATION UNSPEC
Tuberculosis	011.91	UNSPEC PULM TB, BACTERIO/HISTO NOT DONE
Tuberculosis	011.92	UNSPEC PULM TB, BACTERIO/HISTO RESULTS UNKNOWN
Tuberculosis	011.93	UNSPEC PULM TB, BACILLI FOUND IN SPUTUM BY MICRO
Tuberculosis	011.94	UNSPEC PULM TB, BACILLI NOT IN SPUTUM BY MICRO BUT BY BACT CX
Tuberculosis	011.95	UNSPEC PULM TB, BACILLI NOT BY BACTERIO EXAM BUT HISTO
Tuberculosis	011.96	UNSPEC PULM TB, BACILLI NOT BY BACTERIO/HISTO BUT OTH METHOD
Tuberculosis	012	OTH RESPIRATORY TB
Tuberculosis	012.0	PLEURISY
Tuberculosis	012.00	PLEURISY, CONFIRMATION UNSPEC
Tuberculosis	012.01	PLEURISY, BACTERIO/HISTO NOT DONE
Tuberculosis	012.02	PLEURISY, BACTERIO/HISTO RESULTS UNKNOWN
Tuberculosis	012.03	PLEURISY, BACILLI FOUND IN SPUTUM BY MICRO
Tuberculosis	012.04	PLEURISY, BACILLI NOT IN SPUTUM BY MICRO BUT BY BACT CX
Tuberculosis	012.05	PLEURISY, BACILLI NOT BY BACTERIO EXAM BUT HISTO
Tuberculosis	012.06	PLEURISY, BACILLI NOT BY BACTERIO/HISTO BUT OTH METHOD
Tuberculosis	012.1	TB OF INTRATHORACIC LYMPH NODES
Tuberculosis	012.10	TB OF INTRATHORACIC LYMPH NODES, CONFIRMATION UNSPEC
Tuberculosis	012.11	TB OF INTRATHORACIC LYMPH NODES, BACTERIO/HISTO NOT DONE
Tuberculosis	012.12	TB OF INTRATHORACIC LYMPH NODES, BACTERIO/HISTO RESULTS UNKNOWN
Tuberculosis	012.13	TB OF INTRATHORACIC LYMPH NODES, BACILLI FOUND IN SPUTUM BY MICRO
Tuberculosis	012.14	TB OF INTRATHORACIC LYMPH NODES, BACILLI NOT IN SPUTUM BY MICRO BUT BY BACT CX

Tuberculosis	012.15	TB OF INTRATHORACIC LYMPH NODES, BACILLI NOT BY BACTERIO EXAM BUT HISTO
Tuberculosis	012.16	TB OF INTRATHORACIC LYMPH NODES, BACILLI NOT BY BACTERIO/HISTO BUT OTH METHOD
Tuberculosis	012.2	ISOLATED TRACH OR BRONCH TB
Tuberculosis	012.20	ISOLATED TRACH OR BRONCH TB, UNSPEC EXAM
Tuberculosis	012.21	ISOLATED TRACH OR BRONCH TB, BACTERIO/HISTO NOT DONE
Tuberculosis	012.22	ISOLATED TRACH OR BRONCH TB, BACTERIO/HISTO RESULTS UNKNOWN
Tuberculosis	012.23	ISOLATED TRACH OR BRONCH TB, BACILLI FOUND IN SPUTUM BY MICRO
Tuberculosis	012.24	ISOLATED TRACH OR BRONCH TB, BACILLI NOT IN SPUTUM BY MICRO BUT BY BACT CX
Tuberculosis	012.25	ISOLATED TRACH OR BRONCH TB, BACILLI NOT BY BACTERIO EXAM BUT HISTO
Tuberculosis	012.26	ISOLATED TRACH OR BRONCH TB, BACILLI NOT BY BACTERIO/HISTO BUT OTH METHOD
Tuberculosis	012.3	TB LARYNGITIS
Tuberculosis	012.30	TB LARYNGITIS, UNSPEC EXAM
Tuberculosis	012.31	TB LARYNGITIS, BACTERIO/HISTO NOT DONE
Tuberculosis	012.32	TB LARYNGITIS, BACTERIO/HISTO RESULTS UNKNOWN
Tuberculosis	012.33	TB LARYNGITIS, BACILLI FOUND IN SPUTUM BY MICRO
Tuberculosis	012.34	TB LARYNGITIS, BACILLI NOT IN SPUTUM BY MICRO BUT BY BACT CX
Tuberculosis	012.35	TB LARYNGITIS, BACILLI NOT BY BACTERIO EXAM BUT HISTO
Tuberculosis	012.36	TB LARYNGITIS, BACILLI NOT BY BACTERIO/HISTO BUT OTH METHOD
Tuberculosis	012.8	OTH SPEC RESPIRATORY TB
Tuberculosis	012.80	OTH SPEC RESPIRATORY TB, UNSPEC EXAM
Tuberculosis	012.81	OTH SPEC RESPIRATORY TB, BACTERIO/HISTO NOT DONE
Tuberculosis	012.82	OTH SPEC RESPIRATORY TB, BACTERIO/HISTO RESULTS UNKNOWN
Tuberculosis	012.83	OTH SPEC RESPIRATORY TB, BACILLI FOUND IN SPUTUM BY MICRO
Tuberculosis	012.84	OTH SPEC RESPIRATORY TB, BACILLI NOT IN SPUTUM BY MICRO BUT BY BACT CX
Tuberculosis	012.85	OTH SPEC RESPIRATORY TB, BACILLI NOT BY BACTERIO EXAM BUT HISTO
Tuberculosis	012.86	OTH SPEC RESPIRATORY TB, BACILLI NOT BY BACTERIO/HISTO BUT OTH METHOD
Tuberculosis	013	TB OF MENINGES AND CNS
Tuberculosis	013.0	TB MENINGITIS
Tuberculosis	013.00	TB MENINGITIS, UNSPEC EXAM
Tuberculosis	013.01	TB MENINGITIS, BACTERIO/HISTO NOT DONE
Tuberculosis	013.02	TB MENINGITIS, BACTERIO/HISTO RESULTS UNKNOWN
Tuberculosis	013.03	TB MENINGITIS, BACILLI FOUND IN SPUTUM BY MICRO
Tuberculosis	013.04	TB MENINGITIS, BACILLI NOT IN SPUTUM BY MICRO BUT BY BACT CX
Tuberculosis	013.05	TB MENINGITIS, BACILLI NOT BY BACTERIO EXAM BUT HISTO

Tuberculosis	013.06	TB MENINGITIS, BACILLI NOT BY BACTERIO/HISTO BUT OTH METHOD
Tuberculosis	013.1	TUBERCULOMA OF MENINGES
Tuberculosis	013.10	TUBERCULOMA OF MENINGES, UNSPEC EXAM
Tuberculosis	013.11	TUBERCULOMA OF MENINGES, BACTERIO/HISTO NOT DONE
Tuberculosis	013.12	TUBERCULOMA OF MENINGES, BACTERIO/HISTO RESULTS UNKNOWN
Tuberculosis	013.13	TUBERCULOMA OF MENINGES, BACILLI FOUND IN SPUTUM BY MICRO
Tuberculosis	013.14	TUBERCULOMA OF MENINGES, BACILLI NOT IN SPUTUM BY MICRO BUT BY BACT CX
Tuberculosis	013.15	TUBERCULOMA OF MENINGES, BACILLI NOT BY BACTERIO EXAM BUT HISTO
Tuberculosis	013.16	TUBERCULOMA OF MENINGES, BACILLI NOT BY BACTERIO/HISTO BUT OTH METHOD
Tuberculosis	013.2	TUBERCULOMA OF BRAIN
Tuberculosis	013.20	TUBERCULOMA OF BRAIN, UNSPEC EXAM
Tuberculosis	013.21	TUBERCULOMA OF BRAIN, BACTERIO/HISTO NOT DONE
Tuberculosis	013.22	TUBERCULOMA OF BRAIN, BACTERIO/HISTO RESULTS UNKNOWN
Tuberculosis	013.23	TUBERCULOMA OF BRAIN, BACILLI FOUND IN SPUTUM BY MICRO
Tuberculosis	013.24	TUBERCULOMA OF BRAIN, BACILLI NOT IN SPUTUM BY MICRO BUT BY BACT CX
Tuberculosis	013.25	TUBERCULOMA OF BRAIN, BACILLI NOT BY BACTERIO EXAM BUT HISTO
Tuberculosis	013.26	TUBERCULOMA OF BRAIN, BACILLI NOT BY BACTERIO/HISTO BUT OTH METHOD
Tuberculosis	013.3	TB ABSCESS OF BRAIN
Tuberculosis	013.30	TB ABSCESS OF BRAIN, UNSPEC EXAM
Tuberculosis	013.31	TB ABSCESS OF BRAIN, BACTERIO/HISTO NOT DONE
Tuberculosis	013.32	TB ABSCESS OF BRAIN, BACTERIO/HISTO RESULTS UNKNOWN
Tuberculosis	013.33	TB ABSCESS OF BRAIN, BACILLI FOUND IN SPUTUM BY MICRO
Tuberculosis	013.34	TB ABSCESS OF BRAIN, BACILLI NOT IN SPUTUM BY MICRO BUT BY BACT CX
Tuberculosis	013.35	TB ABSCESS OF BRAIN, BACILLI NOT BY BACTERIO EXAM BUT HISTO
Tuberculosis	013.36	TB ABSCESS OF BRAIN, BACILLI NOT BY BACTERIO/HISTO BUT OTH METHOD
Tuberculosis	013.4	TUBERCULOMA OF SPINAL CORD
Tuberculosis	013.40	TUBERCULOMA OF SPINAL CORD, UNSPEC EXAM
Tuberculosis	013.41	TUBERCULOMA OF SPINAL CORD, BACTERIO/HISTO NOT DONE
Tuberculosis	013.42	TUBERCULOMA OF SPINAL CORD, BACTERIO/HISTO RESULTS UNKNOWN
Tuberculosis	013.43	TUBERCULOMA OF SPINAL CORD, BACILLI FOUND IN SPUTUM BY MICRO
Tuberculosis	013.44	TUBERCULOMA OF SPINAL CORD, BACILLI NOT IN SPUTUM BY MICRO BUT BY BACT CX
Tuberculosis	013.45	TUBERCULOMA OF SPINAL CORD, BACILLI NOT BY BACTERIO EXAM BUT HISTO
Tuberculosis	013.46	TUBERCULOMA OF SPINAL CORD, BACILLI NOT BY BACTERIO/HISTO BUT OTH METHOD
Tuberculosis	013.5	TB ABSCESS OF SPINAL CORD
Tuberculosis	013.50	TB ABSCESS OF SPINAL CORD, UNSPEC EXAM

Tuberculosis	013.51	TB ABSCESS OF SPINAL CORD, BACTERIO/HISTO NOT DONE
Tuberculosis	013.52	TB ABSCESS OF SPINAL CORD, BACTERIO/HISTO RESULTS UNKNOWN
Tuberculosis	013.53	TB ABSCESS OF SPINAL CORD, BACILLI FOUND IN SPUTUM BY MICRO
Tuberculosis	013.54	TB ABSCESS OF SPINAL CORD, BACILLI NOT IN SPUTUM BY MICRO BUT BY BACT CX
Tuberculosis	013.55	TB ABSCESS OF SPINAL CORD, BACILLI NOT BY BACTERIO EXAM BUT HISTO
Tuberculosis	013.56	TB ABSCESS OF SPINAL CORD, BACILLI NOT BY BACTERIO/HISTO BUT OTH METHOD
Tuberculosis	013.6	TB ENCEPHALITIS OR MYELITIS
Tuberculosis	013.60	TB ENCEPHALITIS OR MYELITIS, UNSPEC EXAM
Tuberculosis	013.61	TB ENCEPHALITIS OR MYELITIS, BACTERIO/HISTO NOT DONE
Tuberculosis	013.62	TB ENCEPHALITIS OR MYELITIS, BACTERIO/HISTO RESULTS UNKNOWN
Tuberculosis	013.63	TB ENCEPHALITIS OR MYELITIS, BACILLI FOUND IN SPUTUM BY MICRO
Tuberculosis	013.64	TB ENCEPHALITIS OR MYELITIS, BACILLI NOT IN SPUTUM BY MICRO BUT BY BACT CX
Tuberculosis	013.65	TB ENCEPHALITIS OR MYELITIS, BACILLI NOT BY BACTERIO EXAM BUT HISTO
Tuberculosis	013.66	TB ENCEPHALITIS OR MYELITIS, BACILLI NOT BY BACTERIO/HISTO BUT OTH METHOD
Tuberculosis	013.8	OTH SPEC TB OF CNS
Tuberculosis	013.80	OTH SPEC TB OF CNS, UNSPEC EXAM
Tuberculosis	013.81	OTH SPEC TB OF CNS, BACTERIO/HISTO NOT DONE
Tuberculosis	013.82	OTH SPEC TB OF CNS, BACTERIO/HISTO RESULTS UNKNOWN
Tuberculosis	013.83	OTH SPEC TB OF CNS, BACILLI FOUND IN SPUTUM BY MICRO
Tuberculosis	013.84	OTH SPEC TB OF CNS, BACILLI NOT IN SPUTUM BY MICRO BUT BY BACT CX
Tuberculosis	013.85	OTH SPEC TB OF CNS, BACILLI NOT BY BACTERIO EXAM BUT HISTO
Tuberculosis	013.86	OTH SPEC TB OF CNS, BACILLI NOT BY BACTERIO/HISTO BUT OTH METHOD
Tuberculosis	013.9	UNSPEC TB OF CNS
Tuberculosis	013.90	UNSPEC TB OF CNS, UNSPEC EXAM
Tuberculosis	013.91	UNSPEC TB OF CNS, BACTERIO/HISTO NOT DONE
Tuberculosis	013.92	UNSPEC TB OF CNS, BACTERIO/HISTO RESULTS UNKNOWN
Tuberculosis	013.93	UNSPEC TB OF CNS, BACILLI FOUND IN SPUTUM BY MICRO
Tuberculosis	013.94	UNSPEC TB OF CNS, BACILLI NOT IN SPUTUM BY MICRO BUT BY BACT CX
Tuberculosis	013.95	UNSPEC TB OF CNS, BACILLI NOT BY BACTERIO EXAM BUT HISTO
Tuberculosis	013.96	UNSPEC TB OF CNS, BACILLI NOT BY BACTERIO/HISTO BUT OTH METHOD
Tuberculosis	014	TB OF INTESTINES, PERITONEUM, AND MESENTERIC GLANDS
Tuberculosis	014.0	TB PERITONITIS
Tuberculosis	014.00	TB PERITONITIS, UNSPEC EXAM
Tuberculosis	014.01	TB PERITONITIS, BACTERIO/HISTO NOT DONE
Tuberculosis	014.02	TB PERITONITIS, BACTERIO/HISTO RESULTS UNKNOWN

Tuberculosis	014.03	TB PERITONITIS, BACILLI FOUND IN SPUTUM BY MICRO
Tuberculosis	014.04	TB PERITONITIS, BACILLI NOT IN SPUTUM BY MICRO BUT BY BACT CX
Tuberculosis	014.05	TB PERITONITIS, BACILLI NOT BY BACTERIO EXAM BUT HISTO
Tuberculosis	014.06	TB PERITONITIS, BACILLI NOT BY BACTERIO/HISTO BUT OTH METHOD
Tuberculosis	014.8	OTH TB OF INTESTINES, PERITONEUM AND MESENTERIC GLANDS
Tuberculosis	014.80	OTH TB INTEST AND MESEN GLANDS, UNSPEC EXAM
Tuberculosis	014.81	OTH TB INTEST AND MESEN GLANDS, BACTERIO/HISTO NOT DONE
Tuberculosis	014.82	OTH TB INTEST AND MESEN GLANDS, BACTERIO/HISTO RESULTS UNKNOWN
Tuberculosis	014.83	OTH TB INTEST AND MESEN GLANDS, BACILLI FOUND IN SPUTUM BY MICRO
Tuberculosis	014.84	OTH TB INTEST AND MESEN GLANDS, BACILLI NOT IN SPUTUM BY MICRO BUT BY BACT CX
Tuberculosis	014.85	OTH TB INTEST AND MESEN GLANDS, BACILLI NOT BY BACTERIO EXAM BUT HISTO
Tuberculosis	014.86	OTH TB INTEST AND MESEN GLANDS, BACILLI NOT BY BACTERIO/HISTO BUT OTH METHOD
Tuberculosis	015	TB OF BONES AND JOINTS
Tuberculosis	015.0	TB OF VERTEBRAL COLUMN
Tuberculosis	015.00	TB OF VERTEBRAL COLUMN, UNSPEC EXAM
Tuberculosis	015.01	TB OF VERTEBRAL COLUMN, BACTERIO/HISTO NOT DONE
Tuberculosis	015.02	TB OF VERTEBRAL COLUMN, BACTERIO/HISTO RESULTS UNKNOWN
Tuberculosis	015.03	TB OF VERTEBRAL COLUMN, BACILLI FOUND IN SPUTUM BY MICRO
Tuberculosis	015.04	TB OF VERTEBRAL COLUMN, BACILLI NOT IN SPUTUM BY MICRO BUT BY BACT CX
Tuberculosis	015.05	TB OF VERTEBRAL COLUMN, BACILLI NOT BY BACTERIO EXAM BUT HISTO
Tuberculosis	015.06	TB OF VERTEBRAL COLUMN, BACILLI NOT BY BACTERIO/HISTO BUT OTH METHOD
Tuberculosis	015.1	TB OF HIP
Tuberculosis	015.10	TB OF HIP, UNSPEC EXAM
Tuberculosis	015.11	TB OF HIP, BACTERIO/HISTO NOT DONE
Tuberculosis	015.12	TB OF HIP, BACTERIO/HISTO RESULTS UNKNOWN
Tuberculosis	015.13	TB OF HIP, BACILLI FOUND IN SPUTUM BY MICRO
Tuberculosis	015.14	TB OF HIP, BACILLI NOT IN SPUTUM BY MICRO BUT BY BACT CX
Tuberculosis	015.15	TB OF HIP, BACILLI NOT BY BACTERIO EXAM BUT HISTO
Tuberculosis	015.16	TB OF HIP, BACILLI NOT BY BACTERIO/HISTO BUT OTH METHOD
Tuberculosis	015.2	TB OF KNEE
Tuberculosis	015.20	TB OF KNEE, UNSPEC EXAM
Tuberculosis	015.21	TB OF KNEE, BACTERIO/HISTO NOT DONE
Tuberculosis	015.22	TB OF KNEE, BACTERIO/HISTO RESULTS UNKNOWN
Tuberculosis	015.23	TB OF KNEE, BACILLI FOUND IN SPUTUM BY MICRO
Tuberculosis	015.24	TB OF KNEE, BACILLI NOT IN SPUTUM BY MICRO BUT BY BACT CX

Tuberculosis	015.25	TB OF KNEE, BACILLI NOT BY BACTERIO EXAM BUT HISTO
Tuberculosis	015.26	TB OF KNEE, BACILLI NOT BY BACTERIO/HISTO BUT OTH METHOD
Tuberculosis	015.5	TB OF LIMB BONES
Tuberculosis	015.50	TB OF LIMB BONES, UNSPEC EXAM
Tuberculosis	015.51	TB OF LIMB BONES, BACTERIO/HISTO NOT DONE
Tuberculosis	015.52	TB OF LIMB BONES, BACTERIO/HISTO RESULTS UNKNOWN
Tuberculosis	015.53	TB OF LIMB BONES, BACILLI FOUND IN SPUTUM BY MICRO
Tuberculosis	015.54	TB OF LIMB BONES, BACILLI NOT IN SPUTUM BY MICRO BUT BY BACT CX
Tuberculosis	015.55	TB OF LIMB BONES, BACILLI NOT BY BACTERIO EXAM BUT HISTO
Tuberculosis	015.56	TB OF LIMB BONES, BACILLI NOT BY BACTERIO/HISTO BUT OTH METHOD
Tuberculosis	015.6	TB OF MASTOID
Tuberculosis	015.60	TB OF MASTOID, UNSPEC EXAM
Tuberculosis	015.61	TB OF MASTOID, BACTERIO/HISTO NOT DONE
Tuberculosis	015.62	TB OF MASTOID, BACTERIO/HISTO RESULTS UNKNOWN
Tuberculosis	015.63	TB OF MASTOID, BACILLI FOUND IN SPUTUM BY MICRO
Tuberculosis	015.64	TB OF MASTOID, BACILLI NOT IN SPUTUM BY MICRO BUT BY BACT CX
Tuberculosis	015.65	TB OF MASTOID, BACILLI NOT BY BACTERIO EXAM BUT HISTO
Tuberculosis	015.66	TB OF MASTOID, BACILLI NOT BY BACTERIO/HISTO BUT OTH METHOD
Tuberculosis	015.7	TB OF OTH SPEC BONE
Tuberculosis	015.70	TB OF OTH SPEC BONE, UNSPEC EXAM
Tuberculosis	015.71	TB OF OTH SPEC BONE, BACTERIO/HISTO NOT DONE
Tuberculosis	015.72	TB OF OTH SPEC BONE, BACTERIO/HISTO RESULTS UNKNOWN
Tuberculosis	015.73	TB OF OTH SPEC BONE, BACILLI FOUND IN SPUTUM BY MICRO
Tuberculosis	015.74	TB OF OTH SPEC BONE, BACILLI NOT IN SPUTUM BY MICRO BUT BY BACT CX
Tuberculosis	015.75	TB OF OTH SPEC BONE, BACILLI NOT BY BACTERIO EXAM BUT HISTO
Tuberculosis	015.76	TB OF OTH SPEC BONE, BACILLI NOT BY BACTERIO/HISTO BUT OTH METHOD
Tuberculosis	015.8	TB OF OTH SPEC JOINT
Tuberculosis	015.80	TB OF OTH SPEC JOINT, UNSPEC EXAM
Tuberculosis	015.81	TB OF OTH SPEC JOINT, BACTERIO/HISTO NOT DONE
Tuberculosis	015.82	TB OF OTH SPEC JOINT, BACTERIO/HISTO RESULTS UNKNOWN
Tuberculosis	015.83	TB OF OTH SPEC JOINT, BACILLI FOUND IN SPUTUM BY MICRO
Tuberculosis	015.84	TB OF OTH SPEC JOINT, BACILLI NOT IN SPUTUM BY MICRO BUT BY BACT CX
Tuberculosis	015.85	TB OF OTH SPEC JOINT, BACILLI NOT BY BACTERIO EXAM BUT HISTO
Tuberculosis	015.86	TB OF OTH SPEC JOINT, BACILLI NOT BY BACTERIO/HISTO BUT OTH METHOD
Tuberculosis	015.9	TB OF UNSPEC BONES AND JOINTS

Tuberculosis	015.90	TB OF UNSPEC BONES AND JOINTS, UNSPEC EXAM
Tuberculosis	015.91	TB OF UNSPEC BONES AND JOINTS, BACTERIO/HISTO NOT DONE
Tuberculosis	015.92	TB OF UNSPEC BONES AND JOINTS, BACTERIO/HISTO RESULTS UNKNOWN
Tuberculosis	015.93	TB OF UNSPEC BONES AND JOINTS, BACILLI FOUND IN SPUTUM BY MICRO
Tuberculosis	015.94	TB OF UNSPEC BONES AND JOINTS, BACILLI NOT IN SPUTUM BY MICRO BUT BY BACT CX
Tuberculosis	015.95	TB OF UNSPEC BONES AND JOINTS, BACILLI NOT BY BACTERIO EXAM BUT HISTO
Tuberculosis	015.96	TB OF UNSPEC BONES AND JOINTS, BACILLI NOT BY BACTERIO/HISTO BUT OTH METHOD
Tuberculosis	016	TB OF GENITOURINARY SYSTEM
Tuberculosis	016.0	TB OF KIDNEY
Tuberculosis	016.00	TB OF KIDNEY, UNSPEC EXAM
Tuberculosis	016.01	TB OF KIDNEY, BACTERIO/HISTO NOT DONE
Tuberculosis	016.02	TB OF KIDNEY, BACTERIO/HISTO RESULTS UNKNOWN
Tuberculosis	016.03	TB OF KIDNEY, BACILLI FOUND IN SPUTUM BY MICRO
Tuberculosis	016.04	TB OF KIDNEY, BACILLI NOT IN SPUTUM BY MICRO BUT BY BACT CX
Tuberculosis	016.05	TB OF KIDNEY, BACILLI NOT BY BACTERIO EXAM BUT HISTO
Tuberculosis	016.06	TB OF KIDNEY, BACILLI NOT BY BACTERIO/HISTO BUT OTH METHOD
Tuberculosis	016.1	TB OF BLADDER
Tuberculosis	016.10	TB OF BLADDER, UNSPEC EXAM
Tuberculosis	016.11	TB OF BLADDER, BACTERIO/HISTO NOT DONE
Tuberculosis	016.12	TB OF BLADDER, BACTERIO/HISTO RESULTS UNKNOWN
Tuberculosis	016.13	TB OF BLADDER, BACILLI FOUND IN SPUTUM BY MICRO
Tuberculosis	016.14	TB OF BLADDER, BACILLI NOT IN SPUTUM BY MICRO BUT BY BACT CX
Tuberculosis	016.15	TB OF BLADDER, BACILLI NOT BY BACTERIO EXAM BUT HISTO
Tuberculosis	016.16	TB OF BLADDER, BACILLI NOT BY BACTERIO/HISTO BUT OTH METHOD
Tuberculosis	016.2	TB OF URETER
Tuberculosis	016.20	TB OF URETER, UNSPEC EXAM
Tuberculosis	016.21	TB OF URETER, BACTERIO/HISTO NOT DONE
Tuberculosis	016.22	TB OF URETER, BACTERIO/HISTO RESULTS UNKNOWN
Tuberculosis	016.23	TB OF URETER, BACILLI FOUND IN SPUTUM BY MICRO
Tuberculosis	016.24	TB OF URETER, BACILLI NOT IN SPUTUM BY MICRO BUT BY BACT CX
Tuberculosis	016.25	TB OF URETER, BACILLI NOT BY BACTERIO EXAM BUT HISTO
Tuberculosis	016.26	TB OF URETER, BACILLI NOT BY BACTERIO/HISTO BUT OTH METHOD
Tuberculosis	016.3	TB OF OTH URINARY ORGANS
Tuberculosis	016.30	TB OF OTH URINARY ORGANS, UNSPEC EXAM
Tuberculosis	016.31	TB OF OTH URINARY ORGANS, BACTERIO/HISTO NOT DONE

Tuberculosis	016.32	TB OF OTH URINARY ORGANS, BACTERIO/HISTO RESULTS UNKNOWN
Tuberculosis	016.33	TB OF OTH URINARY ORGANS, BACILLI FOUND IN SPUTUM BY MICRO
Tuberculosis	016.34	TB OF OTH URINARY ORGANS, BACILLI NOT IN SPUTUM BY MICRO BUT BY BACT CX
Tuberculosis	016.35	TB OF OTH URINARY ORGANS, BACILLI NOT BY BACTERIO EXAM BUT HISTO
Tuberculosis	016.36	TB OF OTH URINARY ORGANS, BACILLI NOT BY BACTERIO/HISTO BUT OTH METHOD
Tuberculosis	016.4	TB OF EPIDIDYMIS
Tuberculosis	016.40	TB OF EPIDIDYMIS, UNSPEC EXAM
Tuberculosis	016.41	TB OF EPIDIDYMIS, BACTERIO/HISTO NOT DONE
Tuberculosis	016.42	TB OF EPIDIDYMIS, BACTERIO/HISTO RESULTS UNKNOWN
Tuberculosis	016.43	TB OF EPIDIDYMIS, BACILLI FOUND IN SPUTUM BY MICRO
Tuberculosis	016.44	TB OF EPIDIDYMIS, BACILLI NOT IN SPUTUM BY MICRO BUT BY BACT CX
Tuberculosis	016.45	TB OF EPIDIDYMIS, BACILLI NOT BY BACTERIO EXAM BUT HISTO
Tuberculosis	016.46	TB OF EPIDIDYMIS, BACILLI NOT BY BACTERIO/HISTO BUT OTH METHOD
Tuberculosis	016.5	TB OF OTH MALE GENITAL ORGANS
Tuberculosis	016.50	TB OF OTH MALE GENITAL ORGANS, UNSPEC EXAM
Tuberculosis	016.51	TB OF OTH MALE GENITAL ORGANS, BACTERIO/HISTO NOT DONE
Tuberculosis	016.52	TB OF OTH MALE GENITAL ORGANS, BACTERIO/HISTO RESULTS UNKNOWN
Tuberculosis	016.53	TB OF OTH MALE GENITAL ORGANS, BACILLI FOUND IN SPUTUM BY MICRO
Tuberculosis	016.54	TB OF OTH MALE GENITAL ORGANS, BACILLI NOT IN SPUTUM BY MICRO BUT BY BACT CX
Tuberculosis	016.55	TB OF OTH MALE GENITAL ORGANS, BACILLI NOT BY BACTERIO EXAM BUT HISTO
Tuberculosis	016.56	TB OF OTH MALE GENITAL ORGANS, BACILLI NOT BY BACTERIO/HISTO BUT OTH METHOD
Tuberculosis	016.6	TB OOPHORITIS AND SALPINGITIS
Tuberculosis	016.60	TB OOPHORITIS AND SALPINGITIS, UNSPEC EXAM
Tuberculosis	016.61	TB OOPHORITIS AND SALPINGITIS, BACTERIO/HISTO NOT DONE
Tuberculosis	016.62	TB OOPHORITIS AND SALPINGITIS, BACTERIO/HISTO RESULTS UNKNOWN
Tuberculosis	016.63	TB OOPHORITIS AND SALPINGITIS, BACILLI FOUND IN SPUTUM BY MICRO
Tuberculosis	016.64	TB OOPHORITIS AND SALPINGITIS, BACILLI NOT IN SPUTUM BY MICRO BUT BY BACT CX
Tuberculosis	016.65	TB OOPHORITIS AND SALPINGITIS, BACILLI NOT BY BACTERIO EXAM BUT HISTO
Tuberculosis	016.66	TB OOPHORITIS AND SALPINGITIS, BACILLI NOT BY BACTERIO/HISTO BUT OTH METHOD
Tuberculosis	016.7	TB OF OTH FEMALE GENITAL ORGANS
Tuberculosis	016.70	TB OF OTH FEMALE GENITAL ORGANS, UNSPEC EXAM
Tuberculosis	016.71	TB OF OTH FEMALE GENITAL ORGANS, BACTERIO/HISTO NOT DONE
Tuberculosis	016.72	TB OF OTH FEMALE GENITAL ORGANS, BACTERIO/HISTO RESULTS UNKNOWN
Tuberculosis	016.73	TB OF OTH FEMALE GENITAL ORGANS, BACILLI FOUND IN SPUTUM BY MICRO
Tuberculosis	016.74	TB OF OTH FEMALE GENITAL ORGANS, BACILLI NOT IN SPUTUM BY MICRO BUT BY BACT

CX

Tuberculosis	016.75	TB OF OTH FEMALE GENITAL ORGANS, BACILLI NOT BY BACTERIO EXAM BUT HISTO
Tuberculosis	016.76	TB OF OTH FEMALE GENITAL ORGANS, BACILLI NOT BY BACTERIO/HISTO BUT OTH METHOD
Tuberculosis	016.9	GENITOURINARY TB, UNSPEC
Tuberculosis	016.90	UNSPEC GENITOURINARY TB, UNSPEC EXAM
Tuberculosis	016.91	UNSPEC GENITOURINARY TB, BACTERIO/HISTO NOT DONE
Tuberculosis	016.92	UNSPEC GENITOURINARY TB, BACTERIO/HISTO RESULTS UNKNOWN
Tuberculosis	016.93	UNSPEC GENITOURINARY TB, BACILLI FOUND IN SPUTUM BY MICRO
Tuberculosis	016.94	UNSPEC GENITOURINARY TB, TB BA CILLI NOT IN SPUTUM BY MICRO BUT BY BACT CX
Tuberculosis	016.95	UNSPEC GENITOURINARY TB, BACILLI NOT BY BACTERIO EXAM BUT HISTO
Tuberculosis	016.96	UNSPEC GENITOURINARY TB, BACILLI NOT BY BACTERIO/HISTO BUT OTH METHOD
Tuberculosis	017	TB OF OTH ORGANS
Tuberculosis	017.0	TB OF SKIN AND SUBCU TISSUE
Tuberculosis	017.00	TB OF SKIN AND SUBCU TISSUE, UNSPEC EXAM
Tuberculosis	017.01	TB OF SKIN AND SUBCU TISSUE, BACTERIO/HISTO NOT DONE
Tuberculosis	017.02	TB OF SKIN AND SUBCU TISSUE, BACTERIO/HISTO RESULTS UNKNOWN
Tuberculosis	017.03	TB OF SKIN AND SUBCU TISSUE, BACILLI FOUND IN SPUTUM BY MICRO
Tuberculosis	017.04	TB OF SKIN AND SUBCU TISSUE, BACILLI NOT IN SPUTUM BY MICRO BUT BY BACT CX
Tuberculosis	017.05	TB OF SKIN AND SUBCU TISSUE, BACILLI NOT BY BACTERIO EXAM BUT HISTO
Tuberculosis	017.06	TB OF SKIN AND SUBCU TISSUE, BACILLI NOT BY BACTERIO/HISTO BUT OTH METHOD
Tuberculosis	017.1	ERYTHEMA NODOSUM W/HYPERSENS RXN IN TB
Tuberculosis	017.10	ERYTHEMA NODOSUM W/HYPERSENS RXN IN TB, UNSPEC EXAM
Tuberculosis	017.11	ERYTHEMA NODOSUM W/HYPERSENS RXN IN TB, BACTERIO/HISTO NOT DONE
Tuberculosis	017.12	ERYTHEMA NODOSUM W/HYPERSENS RXN IN TB, BACTERIO/HISTO RESULTS UNKNOWN
Tuberculosis	017.13	ERYTHEMA NODOSUM W/HYPERSENS RXN IN TB, BACILLI FOUND IN SPUTUM BY MICRO
Tuberculosis	017.14	ERY NODOSUM W/HYPERSENS RXN IN TB, BACILLI NOT IN SPUTUM BY MICRO BUT BY BACT CX
Tuberculosis	017.15	ERYTHEMA NODOSUM W/HYPERSENS RXN IN TB, BACILLI NOT BY BACTERIO EXAM BUT HISTO
Tuberculosis	017.16	ERY NODOSUM W/HYPERSENS RXN IN TB, BACILLI NOT BY BACTERIO/HISTO BUT OTH METHOD
Tuberculosis	017.2	TB OF PERIPH LYMPH NODES
Tuberculosis	017.20	TB OF PERIPH LYMPH NODES, UNSPEC EXAM
Tuberculosis	017.21	TB OF PERIPH LYMPH NODES, BACTERIO/HISTO NOT DONE
Tuberculosis	017.22	TB OF PERIPH LYMPH NODES, BACTERIO/HISTO RESULTS UNKNOWN

Tuberculosis	017.23	TB OF PERIPH LYMPH NODES, BACILLI FOUND IN SPUTUM BY MICRO
Tuberculosis	017.24	TB OF PERIPH LYMPH NODES, BACILLI NOT IN SPUTUM BY MICRO BUT BY BACT CX
Tuberculosis	017.25	TB OF PERIPH LYMPH NODES, BACILLI NOT BY BACTERIO EXAM BUT HISTO
Tuberculosis	017.26	TB OF PERIPH LYMPH NODES, BACILLI NOT BY BACTERIO/HISTO BUT OTH METHOD
Tuberculosis	017.3	TB OF EYE
Tuberculosis	017.30	TB OF EYE, UNSPEC EXAM
Tuberculosis	017.31	TB OF EYE, BACTERIO/HISTO NOT DONE
Tuberculosis	017.32	TB OF EYE, BACTERIO/HISTO RESULTS UNKNOWN
Tuberculosis	017.33	TB OF EYE, BACILLI FOUND IN SPUTUM BY MICRO
Tuberculosis	017.34	TB OF EYE, BACILLI NOT IN SPUTUM BY MICRO BUT BY BACT CX
Tuberculosis	017.35	TB OF EYE, BACILLI NOT BY BACTERIO EXAM BUT HISTO
Tuberculosis	017.36	TB OF EYE, BACILLI NOT BY BACTERIO/HISTO BUT OTH METHOD
Tuberculosis	017.4	TB OF EAR
Tuberculosis	017.40	TB OF EAR, UNSPEC EXAM
Tuberculosis	017.41	TB OF EAR, BACTERIO/HISTO NOT DONE
Tuberculosis	017.42	TB OF EAR, BACTERIO/HISTO RESULTS UNKNOWN
Tuberculosis	017.43	TB OF EAR, BACILLI FOUND IN SPUTUM BY MICRO
Tuberculosis	017.44	TB OF EAR, BACILLI NOT IN SPUTUM BY MICRO BUT BY BACT CX
Tuberculosis	017.45	TB OF EAR, BACILLI NOT BY BACTERIO EXAM BUT HISTO
Tuberculosis	017.46	TB OF EAR, BACILLI NOT BY BACTERIO/HISTO BUT OTH METHOD
Tuberculosis	017.5	TB OF THYROID GLAND
Tuberculosis	017.50	TB OF THYROID GLAND, UNSPEC ORIGIN
Tuberculosis	017.51	TB OF THYROID GLAND, BACTERIO/HISTO NOT DONE
Tuberculosis	017.52	TB OF THYROID GLAND, BACTERIO/HISTO RESULTS UNKNOWN
Tuberculosis	017.53	TB OF THYROID GLAND, BACILLI FOUND IN SPUTUM BY MICRO
Tuberculosis	017.54	TB OF THYROID GLAND, BACILLI NOT IN SPUTUM BY MICRO BUT BY BACT CX
Tuberculosis	017.55	TB OF THYROID GLAND, BACILLI NOT BY BACTERIO EXAM BUT HISTO
Tuberculosis	017.56	TB OF THYROID GLAND, BACILLI NOT BY BACTERIO/HISTO BUT OTH METHOD
Tuberculosis	017.6	TB OF ADRENAL GLANDS
Tuberculosis	017.60	TB OF ADRENAL GLANDS, UNSPEC EXAM
Tuberculosis	017.61	TB OF ADRENAL GLANDS, BACTERIO/HISTO NOT DONE
Tuberculosis	017.62	TB OF ADRENAL GLANDS, BACTERIO/HISTO RESULTS UNKNOWN
Tuberculosis	017.63	TB OF ADRENAL GLANDS, BACILLI FOUND IN SPUTUM BY MICRO
Tuberculosis	017.64	TB OF ADRENAL GLANDS, BACILLI NOT IN SPUTUM BY MICRO BUT BY BACT CX
Tuberculosis	017.65	TB OF ADRENAL GLANDS, BACILLI NOT BY BACTERIO EXAM BUT HISTO

Tuberculosis	017.66	TB OF ADRENAL GLANDS, BACILLI NOT BY BACTERIO/HISTO BUT OTH METHOD
Tuberculosis	017.7	TB OF SPLEEN
Tuberculosis	017.70	TB OF SPLEEN, UNSPEC EXAM
Tuberculosis	017.71	TB OF SPLEEN, BACTERIO/HISTO NOT DONE
Tuberculosis	017.72	TB OF SPLEEN, BACTERIO/HISTO RESULTS UNKNOWN
Tuberculosis	017.73	TB OF SPLEEN, BACILLI FOUND IN SPUTUM BY MICRO
Tuberculosis	017.74	TB OF SPLEEN, BACILLI NOT IN SPUTUM BY MICRO BUT BY BACT CX
Tuberculosis	017.75	TB OF SPLEEN, BACILLI NOT BY BACTERIO EXAM BUT HISTO
Tuberculosis	017.76	TB OF SPLEEN, BACILLI NOT BY BACTERIO/HISTO BUT OTH METHOD
Tuberculosis	017.8	TB OF ESOPHAGUS
Tuberculosis	017.80	TB OF ESOPHAGUS, UNSPEC EXAM
Tuberculosis	017.81	TB OF ESOPHAGUS, BACTERIO/HISTO NOT DONE
Tuberculosis	017.82	TB OF ESOPHAGUS, BACTERIO/HISTO RESULTS UNKNOWN
Tuberculosis	017.83	TB OF ESOPHAGUS, BACILLI FOUND IN SPUTUM BY MICRO
Tuberculosis	017.84	TB OF ESOPHAGUS, BACILLI NOT IN SPUTUM BY MICRO BUT BY BACT CX
Tuberculosis	017.85	TB OF ESOPHAGUS, BACILLI NOT BY BACTERIO EXAM BUT HISTO
Tuberculosis	017.86	TB OF ESOPHAGUS, BACILLI NOT BY BACTERIO/HISTO BUT OTH METHOD
Tuberculosis	017.9	TB OF OTH SPEC ORGANS
Tuberculosis	017.90	TB OF OTH SPEC ORGANS, UNSPEC EXAM
Tuberculosis	017.91	TB OF OTH SPEC ORGANS, BACTERIO/HISTO NOT DONE
Tuberculosis	017.92	TB OF OTH SPEC ORGANS, BACTERIO/HISTO RESULTS UNKNOWN
Tuberculosis	017.93	TB OF OTH SPEC ORGANS, BACILLI FOUND IN SPUTUM BY MICRO
Tuberculosis	017.94	TB OF OTH SPEC ORGANS, BACILLI NOT IN SPUTUM BY MICRO BUT BY BACT CX
Tuberculosis	017.95	TB OF OTH SPEC ORGANS, BACILLI NOT BY BACTERIO EXAM BUT HISTO
Tuberculosis	017.96	TB OF OTH SPEC ORGANS, BACILLI NOT BY BACTERIO/HISTO BUT OTH METHOD
Tuberculosis	018	MILIARY TB
Tuberculosis	018.0	ACUTE MILIARY TB
Tuberculosis	018.00	ACUTE MILIARY TB, UNSPEC EXAM
Tuberculosis	018.01	ACUTE MILIARY TB, BACTERIO/HISTO NOT DONE
Tuberculosis	018.02	ACUTE MILIARY TB, BACTERIO/HISTO RESULTS UNKNOWN
Tuberculosis	018.03	ACUTE MILIARY TB, BACILLI FOUND IN SPUTUM BY MICRO
Tuberculosis	018.04	ACUTE MILIARY TB, BACILLI NOT IN SPUTUM BY MICRO BUT BY BACT CX
Tuberculosis	018.05	ACUTE MILIARY TB, BACILLI NOT BY BACTERIO EXAM BUT HISTO
Tuberculosis	018.06	ACUTE MILIARY TB, BACILLI NOT BY BACTERIO/HISTO BUT OTH METHOD
Tuberculosis	018.8	OTH SPEC MILIARY TB

Tuberculosis	018.80	OTH SPEC MILIARY TB, UNSPEC EXAM
Tuberculosis	018.81	OTH SPEC MILIARY TB, BACTERIO/HISTO NOT DONE
Tuberculosis	018.82	OTH SPEC MILIARY TB, BACTERIO/HISTO RESULTS UNKNOWN
Tuberculosis	018.83	OTH SPEC MILIARY TB, BACILLI FOUND IN SPUTUM BY MICRO
Tuberculosis	018.84	OTH SPEC MILIARY TB, BACILLI NOT IN SPUTUM BY MICRO BUT BY BACT CX
Tuberculosis	018.85	OTH SPEC MILIARY TB, BACILLI NOT BY BACTERIO EXAM BUT HISTO
Tuberculosis	018.86	OTH SPEC MILIARY TB, BACILLI NOT BY BACTERIO/HISTO BUT OTH METHOD
Tuberculosis	018.9	UNSPEC MILIARY TB
Tuberculosis	018.90	UNSPEC MILIARY TB, UNSPEC EXAM
Tuberculosis	018.91	UNSPEC MILIARY TB, BACTERIO/HISTO NOT DONE
Tuberculosis	018.92	UNSPEC MILIARY TB, BACTERIO/HISTO RESULTS UNKNOWN
Tuberculosis	018.93	UNSPEC MILIARY TB, BACILLI FOUND IN SPUTUM BY MICRO
Tuberculosis	018.94	UNSPEC MILIARY TB, BACILLI NOT IN SPUTUM BY MICRO BUT BY BACT CX
Tuberculosis	018.95	UNSPEC MILIARY TB, BACILLI NOT BY BACTERIO EXAM BUT HISTO
Tuberculosis	018.96	UNSPEC MILIARY TB, BACILLI NOT BY BACTERIO/HISTO BUT OTH METHOD
Tularemia	021	TULAREMIA
Tularemia	021.0	ULCEROGLANDULAR TULAREMIA
Tularemia	021.1	ENTERIC TULAREMIA
Tularemia	021.2	PULM TULAREMIA
Tularemia	021.3	OCULOGLANDULAR TULAREMIA
Tularemia	021.8	OTH SPEC TULAREMIA
Tularemia	021.9	UNSPEC TULAREMIA
Typhoid, Acute	002.0	TYPHOID FEVER
Typhus, Epidemic	080	LOUSE-BORNE (EPIDEMIC) TYPHUS
Vaccinia	999.0	GENERALIZED VACCINIA
Vaccinia	051.0	COWPOX
Vibrio infection, other	005.4	FOOD POISONING DUE TO VIBRIO PARAHAEMOLYTICUS
Vibrio vulnificus	005.81	FOOD POISONING DUE TO VIBRIO VULNIFICUS
Whooping Cough	033.0	WHOOPING COUGH DUE TO BORDETELLA PERTUSSIS (B. PERTUSSIS)
Whooping Cough	484.3	PNEUMONIA IN WHOOPING COUGH
Yellow Fever	060	YELLOW FEVER
Yellow Fever	060.0	SYLVATIC YELLOW FEVER
Yellow Fever	060.1	URBAN YELLOW FEVER
Yellow Fever	060.9	YELLOW FEVER, UNSPEC

Appendix 2: Sample Data Request

Data Request Methodology

Retrospective Cohort Study:

Definition of the cohort: All patients (e.g., outpatients, inpatients, ED patients) at your healthcare facility who were assigned one of the listed ICD9 diagnostic codes for a communicable disease and who were either discharged or had an outpatient visit date during the following time periods: January 1, 1995 to December 31, 1997 and January 1, 2000 to December 31, 2006.

Data collection: For each patient in the cohort, please collect the following data elements (as they are available at your institution) from the department that maintains discharge data (e.g., billing, medical coding, medical records). Please request your data abstracting department to provide you with a line list of these patients with the data in Microsoft Excel format).

For each patient:

a.   Healthcare facility

b.   Name (first, middle, last)*

c.   Hospital identification number*

d.   Social security number

e.   Address

f.   Zip code

g.   County of residence

h.   Date of birth*

i.   Gender

j.   Race

k.   Discharge diagnosis code(s) (ICD-9 codes)*

l.   Discharge diagnosis description*

m.   Procedure codes

n.   Outpatient physician seen, discharge physician seen

o.   Insurance type

p.   Nursing unit

q.   Hospital service

r.   Discharge status

s.   Site of care (i.e., inpatient, outpatient, emergency)

t.   Admission date (for inpatient)*

u.   Discharge date (for inpatient)*

v.   Date of service (for outpatient)*

* Starred data elements are required in order to complete the basic objectives of this study, other data elements are also requested for analysis, but if not available in the discharge data database can be omitted.

Appendix 3: Example Application of Bayes Theorem for Adjustment of ICD-9-CM-based Complete-

ness Studies

		Reported	
		Yes	No
ICD-9 Code for Communi-cable Disease	**CDC Disease**	**A1**	**B1**
	CDC No Disease	**C1=0**	**D1**
No ICD-9 Code for Communi-cable Disease	**CDC Disease**	**A2 (Not Meas-ured)**	**B2 (Not Meas-ured)**
	CDC No Disease	**C2=0**	**D2 (Not Meas-ured)**

R =Reported to the State surveillance system

C =Meets the CDC case definition

I =Assigned an ICD-9-CM code for a communicable disease

$$P(R|C) = \frac{P(C|R)\ P(R)}{P(C)}$$

$$= \frac{P(C|R)\ P(R|I)\ P(I)}{P(C)\quad P(I|R)}$$

$$= \frac{P(C|R)\ P(I|C)\ P(R|I)\ P(I)}{P(C|I)\ P(I)\ \ P(I|R)}$$

$$= \frac{P(C|R)\ P(I|C)\ P(R|I)}{P(I|R)\ P(C|I)}$$

Estimates:

P(C|R)=1, because if a disease is reported it should meet CDC case definition

P(I|C)= sensitivity values estimated = (A1+B1)/(A1+B1+A2+B2)

P(R|I)= completeness proportions estimated

P(I|R) = (A1)/(A1+A2)

P(C|I)= positive predictive values estimated

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