Background. There is limited data on the indirect and non-medical costs associated with congenital cytomegalovirus (cCMV). Attempts to predict the economic impact of disease often rely on secondary analyses of large private databases, and may not capture the full spectrum of a disease. The granularity of billing codes in the Electronic Medical Record (EMR) make it possible to track health outcomes over time, however, with over 80,000 unique codes in ICD-10, selecting the appropriate codes requires specific content knowledge and can lead to bias in categorization. The Systematized Nomenclature of Medicine—Clinical Terms (SNOMED-CT)® provides physicians a tool to find specific ICD-10 on the basis of semantic terms. These terms can be used to build disease state-specific clusters of ICD-10 codes by which to study the economic impact of any disease, including this potentially devastating congenital infection.

Methods. Using a series of data parsing and processing scripts written in SAS V9.4 (Cary, NC), we extracted the diagnosis codes for 190 patients seen in our Congenital Cytomegalovirus Clinic at Texas Children's Hospital in Houston, Texas. This data were consolidated into a relational database of clinical information. Through a second program we developed, clusters of ICD-10 codes were imputed from the SNOMED-CT® on the basis of semantic terms associated with cCMV (e.g., "hearing problem," "developmental disability," "neurological problem").

Results. A total of 190 patients have been seen in our clinic with an ICD-10 diagnosis of CMV infection, 144 of these had cCMV, and 102 of these were born after 1/1/2008 (the inception date of our EMR). 60% of these patients were Caucasian (21% Hispanic), and 25% African American. 54 (53%) had hearing deficits, 17 (16%) had hearing aids, and 55 (54%) had developmental abnormalities. The average time (in years) to development of specific deficits are shown in Figure 1.

Conclusion. The spectrum of disease of cCMV is broad and has been well studied in the past. The EMR gives us the potential to further study this disease in finer detail and identify rates of disease progression by mining the ICD-10 codes associated with these patients throughout time. These results should prove invaluable for generating cost-models for the economic impact of cCMV.

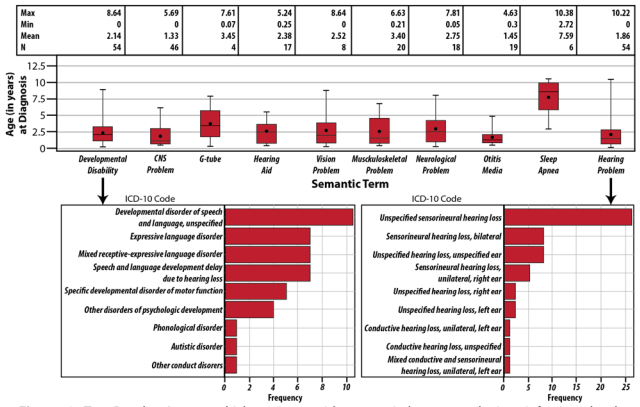

Figure 1: Top Panel - Age at which patients with congenital cytomegalovirus infection develop symptoms within the noted categories. Whisker plots with mean and standard deviation shown. Bottom Panel - Deficits within each system can be broken down into the specific ICD-10 code associated with each diagnosis. The ICD-10 codes that comprise each category are defined by symantic terms imputed from the SNOMED-CT.

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2338. Early Predictors of Mortality in Neonatal Disseminated Herpes Simplex Virus Infection

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Background. Disseminated neonatal herpes simplex virus (dHSV) infection is associated with substantial morbidity and an estimated case fatality rate of ~25% despite antiviral therapy. Contemporary data on predictors of mortality among infants with dHSV infection are limited.

Methods. From January 2012 to December 2018, neonates with HSV infection were identified by the Virology database at Nationwide Children's Hospital. Demographic, clinical, laboratory, and radiographic data were obtained from the infants' electronic healthcare records to identify cases of dHSV infection and to determine possible predictor(s) of mortality. dHSV was defined as detection of HSV DNA by polymerase chain reaction (PCR) in blood, cerebrospinal fluid, or skin/eye/mouth, and evidence of hepatitis, pneumonitis, sepsis, or coagulopathy, with or without central nervous system involvement.

Results. Of 43 neonates with HSV infection, 12 (28%) infants (median [IQR] age: 8.5 [7–11] days) had dHSV and 6 (50%) died. Clinical and laboratory findings of neonates who survived vs. those who died are presented in Table 1. The median duration of symptoms at presentation was 1.5 [1–2] days. Among infants who died, the median duration of hospitalization to time of death was 1.5 days (range, 0 to 4 days). Clinical signs at presentation and blood semiquantiative viral loads (cycle threshold, Ct) were not different between infants who survived (Ct 18.0 [15.4–23.3]) and those who died (16.6 [13.4–23.3]; $P > 0.05$). Initial serum alanine aminotransferase (ALT), INR or lactate were not different between the two groups. However, initial serum median albumin concentration was lower among those who died vs. survivors (1.8 g/dL vs. 2.7 g/dL, $P = 0.004$). To assess the sensitivity and specificity of potential laboratory predictors of mortality, serum laboratory values were evaluated as follows (sensitivity, specificity): ALT > 800 (67%, 80%), INR > 2.7 (67%, 80%), serum lactate > 3 mmol/L (80%, 100%), and initial serum albumin < 2 g/dL (100%, 100%).

Conclusion. Albumin concentrations < 2 g/dL at presentation correlated highly with mortality in neonatal dHSV infection, suggesting that hypoalbuminemia may reflect components of both viral sepsis and poor synthetic liver function. Larger cohorts of neonates with dHSV infection are needed to confirm this result.

Table 1: Clinical and Laboratory Findings Among Neonates with Disseminated HSV Infection

	Total (n=12)	Deceased (n=6)	Survivors (N=6)	p-value
Age, in days, median [IQR]	8.5 [7-11]	9.5 [7-14]	7 [7-11]	0.56
Sex, male, n (%)	8 (67%)	4 (67%)	4 (67%)	>0.99
Clinical findings, n (%)				
Hypoxemia	11 (92%)	6 (100%)	5 (83%)	>0.99
Lethargy	8 (67%)	6 (100%)	2 (33%)	0.06
Fever/Hypothermia	7 (25%)	4 (67%)	3 (50%)	>0.99
Apnea	7 (58%)	4 (67%)	3 (50%)	>0.99
Hepatosplenomegaly	5 (42%)	1 (17%)	4 (67%)	0.24
Rash*	3 (25%)	2 (33%)	1 (17%)	>0.99
Seizure activity	2 (17%)	1 (17%)	1 (17%)	>0.99
Admission Serum Laboratory Results, Median [IQR]				
WBC (10^3 cells/uL)	7.2 [5.2-12.4]	7.5 [5.5-13.5]	6.1 [4.1-12.8]	0.56
ANC (10^3 cells/uL)	2.5[0.7-5.6]	3.6 [0.3-8.5]	2.5 [1.4-4.3]	>0.99
ALC (10^3 cells/uL)	2.2 [1.2-4.0]	2.5 [1.1-4.4]	2.2 [1.4-5.5]	0.94
Hemoglobin (g/dL)	12.8 [9.7-14.9]	12.5 [8.6-14.1]	13 [11.6-16.3]	0.31
Platelets (10^3 /uL)	69 [12-139]	62 [40.3-103]	110 [36-161]	0.45
PT (s)	29.3 [19.4-58.4]	58 [18.8-99]	26.3 [18.7-36.7]	0.25
INR	2.7 [1.6-6.4]	6.4 [1.5-13.3]	2.4 [3.6-1.5]	0.23
PTT (s)	71 [37-250]	165 [36.7-250]	71 [38-72]	0.21
Albumin (g/dL)	2.1 [1.8-2.8]	1.8 [1.2-1.8]	2.7 [2.1-3.1]	**0.004**
ALT (U/L)	825 [68-1715]	1161 [429-1646]	603 [66-2874]	0.93
AST (U/L)	4674 [130-8706]	6829 [2369-10410]	3189 [130-7054]	0.40
Total Bilirubin (mg/dL)	2 [1.2-4.6]	2 [1.6-6.7]	1.7 [0.8-3.7]	0.54
Direct Bilirubin (mg/dL)	0.1 [0-0.8]	0.8 [0.1-1.4]	0 [0-0.4]	0.10
BUN (mg/dL)	21 [14-25]	24 [15-26]	21 [14-24]	0.56
Creatinine (mg/dL)	0.48 [0.39-1.06]	1.06 [0.43-1.27]	0.43 [0.38-0.50]	0.18
Lactate (mmol/L)	2.9 [2.1-9.8]	9.6 [3.9-12.7]	2.2 [1.23-2.7]	0.095

*Vesicular (2), petechial (1)
WBC, white blood cell; ANC, absolute neutrophil count; ALC; absolute lymphocyte count; PT, prothrombin time; PTT, partial thromboplastin time; ALT, alanine aminotransferase; AST, aspartate aminotransferase; BUN, blood urea nitrogen

Disclosures. **All authors:** No reported disclosures.

2339. *Clostridioides difficile*: Impact of Active Screening of Asymptomatic Carriers and Testing Stewardship

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Background. We recently implemented a hospital-wide *C. difficile* testing algorithm and screening/isolation of *C. difficile* asymptomatic carriers primarily in heme-onc units. We aim to evaluate the impact of these interventions on the epidemiology of *C. difficile* + tests.

Methods. This retrospective cohort was performed in a 600-bed hospital in Milwaukee, WI, from January 1, 2016 to March 31, 2019. All clinical *C. difficile* tests included nucleic acid amplification (NAAT; Xpert *C. difficile*, Cepheid). On February 2017, all NAAT+ tests had toxin (tox) checked (Quick check complete, Alere). Testing algorithm (Figure 1) started mid 2016 until now. Screening phases included: Phase 1 (September 2016–May 2017): *C. difficile* screening cultures shared with units but not placed in electronic medical records (EMR). Patients + placed on enteric precautions (gown, gloves, hand hygiene). Phase 2 (May 2017–January 2018): *C. difficile* screening (NAAT) performed on admission and weekly thereafter, results placed in EMR, NAAT+ patients placed on enteric precautions. Phase 3 (January 2018–present): *C. difficile* screening (NAAT) on admission, results placed in EMR, NAAT+ patients placed on enteric precautions. Federal reporting changed to only reporting NAAT+tox+. Tests (NAAT+, NAAT+tox+, and NAAT+tox-) were analyzed using Poisson regression offsetting for log of patient-days using SAS, v9.4.

Results. Hospital-wide *C. difficile* tests decreased from 21 to 10.9 tests per 1,000 patient-days ($P < 0.0001$; Figure 2). This effect was seen in heme-onc units (41 to 15.7; $P < 0.0001$; Figure 3) and in all other units (18.9 to 9.9; $P < 0.0001$). All NAAT+ results decreased from 2.99 to 1.94 per 1,000 patient-days hospital wide ($P < 0.0001$) but remained unchanged in heme-onc units (4.6 to 3.7, $P > 0.05$). NAAT+tox+ results remained unchanged hospital wide and in heme-onc units (0.8 to 0.7 and 1.1 to 1.2,

respectively; both $P > 0.05$); however, the frequency of NAAT+tox– tests decreased hospital wide (1.8 to 1.3; $P = 0.0003$) and in heme-onc units (3.8 to 2.4; $P = 0.05$).

Conclusion. A *C. difficile* testing algorithm was successful decreasing the number of *C. difficile* tests performed and had a hospital-wide reduction of NAAT+tox– tests. The rate of NAAT+tox+ cases in heme-onc units and hospital wide remained unchanged despite active screening and isolation in selected units.

Figure 1. *Clostridioides difficile* testing algorithm

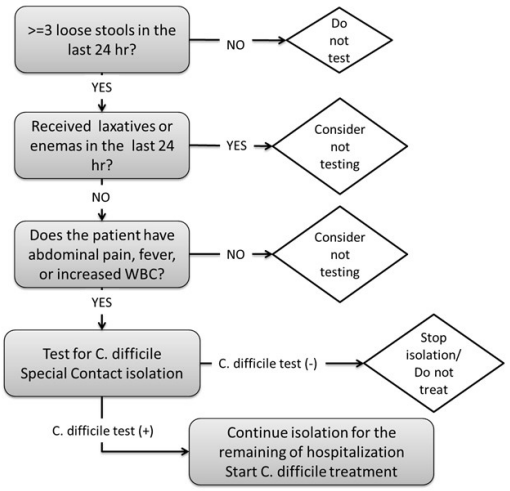
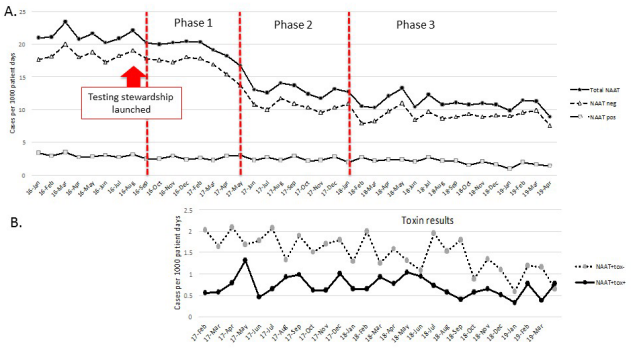
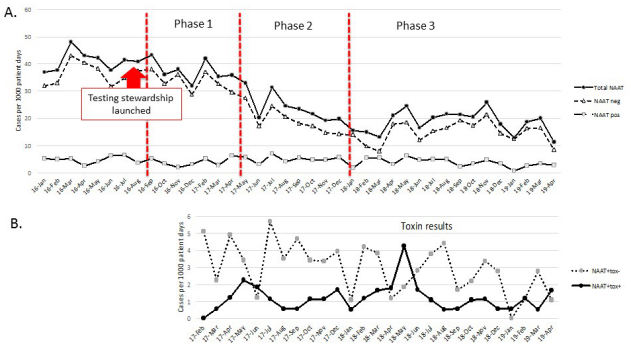


Figure 2. Hospital wide *Clostridioides* difficile test results



A. Nucleic acid amplification test (NAAT) performed and their respective results per 1000 patient days. Phases 1-3 corresponded to different *C. difficile* screening and isolation interventions primarily in hematology-oncology units.
B. NAAT positive results based on the toxin EIA positivity or negativity per 1000 patient days.

Figure 3. Hematology oncology units - *Clostridioides* difficile test results



A. Nucleic acid amplification test (NAAT) performed and their respective results per 1000 patient days. Phases 1-3 corresponded to different *C. difficile* screening and isolation interventions primarily in hematology-oncology units.
B. NAAT positive results based on the toxin EIA positivity or negativity per 1000 patient days.

Disclosures. **All authors:** No reported disclosures.

2340. Diagnostic Stewardship: Survey of Urine Culturing and *C. difficile* Testing Practices Amongst Oregon Microbiology Labs

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Background. Testing for urinary tract infection (UTI) and Clostridiodes difficile infection (CDI) poses diagnostic and antimicrobial stewardship challenges. Both diagnoses hinge on local microbiology laboratory algorithms. For UTI testing, the definition of "abnormal" urinalysis and the use of reflex urine cultures, both of which alter the frequency of bacteriuria detection, likely differs between laboratories. For CDI, pretest probability, choice and sequence of diagnostic tests are likely variable and impact the chances of accurate diagnosis.

Methods. To understand laboratory practices and determine variations in local testing algorithms, we deployed a self-administered survey to microbiology laboratories serving Oregon healthcare facilities via SurveyMonkey in September 2018. Responses were collected through April 2019. We analyzed a subset of questions focused on UTI and CDI diagnosis.

Results. Of 51 surveyed laboratories, response rate was 86% (n = 44). 91% of respondents (n = 40) process bacterial cultures. 47.5% (n = 19) primarily perform urine culture when ordered, whereas the remainder primarily perform cultures in a reflex algorithm when ordered (n = 12; 30%) or a reflex algorithm automatically (n = 9; 22.5%) (Figure 1). The definition of an abnormal urinalysis varied widely (Figure 2). 15% (n = 6) of laboratories reported considering changes to their workflow; two cited a goal of reducing unnecessary testing. Of the 32 laboratories that perform in-house *C. difficile* testing, the assays and sequence in which they were implemented in testing algorithms varied substantially (Figure 3) and most commonly included NAAT testing. Seven (21.8%) laboratories reported recently changed practices; these changes did not favor any particular algorithm. 84.2% (n = 32) reported stool rejection criteria to limit unnecessary testing, but these criteria varied (Figure 4).

Conclusion. Wide variation exists in laboratory workflows for UTI and CDI diagnoses in Oregon, suggesting lack of consensus on optimal practices. Encouragingly, multiple labs described recently implemented or planned interventions to reduce unnecessary testing for both infections. This snapshot will inform statewide education and interventions to optimize testing and help prevent patient and population harm.

Figure 1: Which is the most common circumstance by which urine cultures are performed?

Circumstance	Labs (n = 40)
When urine culture is ordered (as a stand-alone order)	47.5% (19)
Abnormal urinalyses +/- microscopy are reflexed to culture only if ordered	30% (12)
All abnormal UAs +/- microscopy are automatically reflexed to culture	22.5% (9)

Figure 2: Current criteria for abnormal urinalyses and plans for change

If reflex culturing is performed for abnormal UA and/or microscopy, what are the criteria used to define "abnormal" for general adult patients?	
Definition of Abnormal	**Labs utilizing definition (n = 40)**
Positive leukocyte esterase	52.5% (21)
Positive nitrite	55% (22)
WBC >5/HPF	22.5% (9)
WBC >10/HPF	25% (10)
Bacteria present	42.5% (17)
Blood present	5% (2)
Is your laboratory considering changing your UTI testing practice within the next year?	
Considering changes	**Labs (n = 40)**
Yes	15% (6)
No	85% (34)
If considering changes, why?	
N=2 Changing reflex criteria N= 2 Criteria "not stringent enough" N = 2 Algorithm is out of date/needs updating per clinicians	

Figure 3: Current *C. difficile* testing methods utilization and plans for change

C. difficile **testing techniques among labs with in-house testing (n=32)**		
Test Type	**Used as first line (1°) testing**	**Used as routine second line (2°) testing (n = 11)***
Enzyme immunoassay (EIA) Toxin A/B and Antigen (Simultaneous testing)	28.1% (9)	9.1% (1)
Nucleic Acid Amplification Test (NAAT) (e.g., PCR, Illumigene, Luminex, Biofire)	59.3% (19)	63.6% (7)
EIA for Toxin A and/or B only	12.5% (4)	27.3% (3)
Other	0	0
*11 labs perform second line testing. 4 different workflows were identified. Arrows indicate workflow from first to second line testing.		
Has your *C. difficile* lab testing algorithm changed since January 2016? (n=32)		
Yes	21.8% (7)	
No	68.8% (22)	
Unsure or N/A	9.3% (3)	
If yes, what was the previous order of testing?		
Number of Labs	**Current workflow**	**Prior workflow**
2	1° EIA toxin A/B + antigen 2° NAAT	NAAT alone
2	1° NAAT 2° EIA for toxin	NAAT alone
1	1° NAAT 2° EIA toxin A/B + antigen	EIA toxin A/B + antigen alone
1	NAAT	EIA toxin A/B + antigen alone
1	NAAT in-house	NAAT send out